

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 20:19:53 ; Search time 188 Seconds
(without alignments)
624.011 Million cell updates/sec

Title: US-09-803-918a-2
Perfect score: 1362
Sequence: 1 MKAALVTLAVLFTGSGARH.....SPKVSFLSALVEYTKKLTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	267	1 AAP61079	Assumed h
2	1362	100.0	267	1 AAP82128	Entire hu
3	1362	100.0	267	2 AAR72705	Human apo
4	1362	100.0	267	2 AAR34032	Sequence
5	1362	100.0	267	2 AAY18675	Human apo
6	1362	100.0	267	4 AAB47620	Full leng
7	1362	100.0	267	5 AAO15892	Human apo
8	1362	100.0	267	5 ABG97593	Human apo
9	1362	100.0	267	6 ABR44031	Human apo
10	1362	100.0	267	6 ABP57065	Human apo
11	1362	100.0	267	6 ADA61214	Human apo
12	1362	100.0	267	7 ADJ83084	Human apo
13	1362	100.0	267	8 ADI19752	Human apo
14	1362	100.0	267	8 ABM81308	Tumour-as
15	1362	100.0	267	9 ADY75146	Brain tum
16	1362	100.0	267	9 AEA17397	Human pro
17	1362	100.0	267	9 AEA81148	Human apo
18	1362	100.0	267	9 AEB43205	Human apo
19	1362	100.0	275	6 AAO30162	Human apo
20	1359	99.8	267	7 ADJ68447	Human hea
21	1359	99.8	267	7 ADJ83083	Human pro
22	1355	99.5	267	6 ABR44032	Human mut
23	1354	99.4	267	2 AAW08602	Human apo
24	1351.5	99.2	268	1 AAP80668	Recombina

ALIGNMENTS

RESULT 1
AAP61079

ID AAP61079 standard; protein; 267 AA.

AC AAP61079;

XX 25-MAR-2003 (revised)

DT 07-OCT-1991 (first entry)

XX Assumed human apolipoprotein A-1 derivative gene product.

XX Hyperlipaemia; arteriosclerosis.

XX Homo sapiens.

XX JP61096998-A.

PD 15-MAY-1986.

XX 16-OCT-1984; 84JP-00216988.

XX 16-OCT-1984; 84JP-00216988.

XX (MITU) MITSUBISHI CHEM IND LTD.

XX WPI; 1986-165025/26.

XX N-PSDB; AAN60886.

XX Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA fragment in cloning site downstream of expression vector promoter and introducing into host microorganism.

XX Disclosure; Fig 2; 9pp; Japanese.

XX The human apolipoprotein may be produced by a suitable transformed host, it is effective in treating hyperlipaemia and arteriosclerosis. (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 1; Length 267;

Best Local Similarity 100.0%; Pred.No.3.7e-99;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAALVTLAVLFTGSGARHFWQDPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

DB 1 MKAALVTLAVLFTGSGARHFWQDPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDLNLEKETEGLRQEMSKDLEEVKAK 120
 DB 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDLNLEKETEGLRQEMSKDLEEVKAK 120
 QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHQLQEKLSPLGEMMRDRARAHV 180
 DB 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHQLQEKLSPLGEMMRDRARAHV 180
 QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 QY 241 GLLPVLESFKVSFLSALEYTKKLNQ 267
 DB 241 GLLPVLESFKVSFLSALEYTKKLNQ 267

RESULT 2

AAP82128
 ID AAP82128 standard; protein; 267 AA.
 AC AAP82128;

XX 25-MAR-2003 (revised)
 DT 24-OCT-1990 (first entry)

DE Entire human preproapoprotein A1.

XX human preproapoprotein A1; high density lipoprotein deficiency; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= precursor
 FT Peptide 19..24
 FT /label= propeptide
 FT Protein 25..267
 FT /label= mature apoprotein

XX EP293357-A.

XX 30-NOV-1988.

XX 24-MAY-1988; 88EP-00870095.

XX 28-MAY-1987; 87GB-00012540.

XX (UNIO) UCB SA.
 XX (BOLL/) BOLLER A.

XX Bollen A, Gobert J, Wulfert E;

XX WPI; 1988-339891/48.

XX N-PSDB; AAN82064.

XX New DNA encoding human pro-apo-lipoprotein A1 - modified to eliminate hairpin structures.

XX Disclosure; Page ?; 25pp; French.

XX The cDNA 878bp fragment encoding preproapoprotein A1 was detected in Clone pUB1609 derived from human liver cells. See also AAN81258.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 267 AA;

XX Query Match 100.0%; Score 1362; DB 1; Length 267;
 XX Best Local Similarity 100.0%; Pred. No. 3.7e-99;
 XX Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAVLTAVLFLTGSAHFHQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60

DB 1 MKAAVLTAVLFLTGSAHFHQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60
 QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDLNLEKETEGLRQEMSKDLEEVKAK 120
 DB 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPGVTQEFWDLNLEKETEGLRQEMSKDLEEVKAK 120
 QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHQLQEKLSPLGEMMRDRARAHV 180
 DB 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHQLQEKLSPLGEMMRDRARAHV 180
 QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGCGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 QY 241 GLLPVLESFKVSFLSALEYTKKLNQ 267
 DB 241 GLLPVLESFKVSFLSALEYTKKLNQ 267

RESULT 3

AAR72705
 ID AAR72705 standard; protein; 267 AA.
 XX

AC AAR72705;

DT 31-OCT-1995 (first entry)

XX Human apo A-I including signal and propeptide sequences.

XX Apo A-I; LDL cholesterol; low density lipoprotein; lipid.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..18
 FT /label= presignal
 FT Peptide 19..240
 FT /label= claimed
 FT /note= "as part of fusion polypeptide"
 FT Peptide 19..24
 FT /label= propeptide
 FT Peptide 120..135
 FT /label= claimed
 FT /note= "as part of fusion polypeptide"

XX US5408038-A.

XX 18-APR-1995.

XX 08-OCT-1992; 92US-00959946.

XX 09-OCT-1991; 91US-00774633.

XX 18-JUN-1992; 92US-00901706.

XX (SCRI) SCRIPPS RES INST.

XX Witztum JL, Koduri KR, Young SG, Smith RS, Curtiss LK;

XX WPI; 1993-134378/16.

XX N-PSDB; AAQ89634.

XX Polypeptide mimic of native apo B-100 and native apo A-I - useful in assays for LDL and HDL in plasma samples.

XX Claim 10; Fig 2; 41pp; English.

XX AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its corresp. cDNA, including presignal residues and propeptide residues, according to Seilhamer et al., DNA 3(4):309 (1984). A dispersible apo A-1/8-100 fusion polypeptide is claimed which contains a first AA sequence of apo A-I and that includes at least AA sequence positions 120-135 (see AAR72606) and which reacts with pan anti-apo AI antibodies such as: AI-4

CC ATCC HB8744; AI-7 ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI
CC -11 ATCC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB
CC 9204; AI-18 ATCC HB 9507
XX
SQ Sequence 267 AA;
Query Match 100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAAVLTAVLFTGTSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFTGTSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTOEFWDNLEKTEGLRQEMSKOLEEYKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTOEFWDNLEKTEGLRQEMSKOLEEYKAK 120
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
RESULT 4
AAR34032
ID AAR34032 standard; protein; 267 AA.
AC AAR34032;
XX
XX 25-MAR-2003 (revised)
DT 13-AUG-1993 (first entry)
XX
XX
DE Sequence of apo AI.
XX
XX Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
XX
XX Homo sapiens.
XX
XX WO9307165-A1.
XX
XX 15-APR-1993.
XX
XX 09-OCT-1992; 92WO-US008634.
XX
XX 09-OCT-1991; 91US-00774633.
XX
XX 18-JUN-1992; 92US-00901706.
XX
XX 08-OCT-1992; 92US-00959946.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Smith RS, Curtiss LK, Koduri KR, Witztum JL, Young SG;
XX
XX WPI; 1993-134378/16.
XX
XX N-PSDB; AAO40030.
XX
XX Polypeptide mimic of native apo B-100 and native apo A-I - useful in
PT assays for LDL and HDL in plasma samples.
XX
XX Claim 19; Page 105-106; 137pp; English.
XX
XX The inventors claim a portion of the polypeptide contg. apo B-100 that
CC immunoreacts with antibodies secreted by the hybridoma MB47 having ATCC
CC Accession No. 8746. Polypeptides specifically claimed include residues
CC 217-297, 216-310, 216-331, 216-352, 216-377, 1-377, 205-297, 173-297, 140
CC -297. DNA sequences encoding the polypeptides are also claimed. Also

CC claimed are a fusion polypeptide that contains: (a) a first amino
CC acid residue sequence up to 250 residues in length that includes residues
CC 120-135 of apo A-I, (b) a second amino acid residue sequence up to 375
CC residues in length that includes residues 217-297 of apo B-100 and DNA
CC encoding it. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25
CC -MAR-2003 to correct PR field.)
XX
SQ Sequence 267 AA;
Query Match 100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAAVLTAVLFTGTSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFTGTSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTOEFWDNLEKTEGLRQEMSKOLEEYKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTOEFWDNLEKTEGLRQEMSKOLEEYKAK 120
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
RESULT 5
AAV18675
ID AAV18675 standard; protein; 267 AA.
XX
XX AAV18675;
XX
XX 09-JUL-1999 (first entry)
XX
XX Human apolipoprotein AI protein sequence.
XX
XX Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder; ApoA-I;
XX cardiovascular disease; atherosclerosis; restenosis; LCAT;
XX hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
XX
XX Homo sapiens.
XX
XX WO9916409-A2.
XX
XX 08-APR-1999.
XX
XX 28-SEP-1998; 98WO-US020329.
XX
XX 29-SEP-1997; 97US-00940136.
XX
XX (DASS/) DASSEUX J.
XX (SEKU/) SEKUL R.
XX (BUTY/) BUTTNER K.
XX (CORN/) CORNUT I.
XX (METZ/) METZ G.
XX (DUFO/) DUFORCQ J.
XX
XX Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX WPI; 1999-254921/21.
XX N-PSDB; AAX55971.
XX
XX Nucleic acid encoding apoproteinA-I agonist peptides.
XX
XX Example; Fig 1; 232pp; English.
PS

XX The present invention describes a nucleic acid (A) encoding an
 CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A), are
 CC useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
 CC endotoxemia (septic shock). Host cells containing (A) can also be used to
 CC study the role of apoA-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its subpopulation
 CC involved in retrograde cholesterol transport) and for imaging the
 CC circulatory system or HDL accumulations at fatty streaks. The present
 CC sequence represents human apoA-I
 XX
 SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 2; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.7e-99;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFTGSOARHFQWODEPPQSPFWRVKDQATVYVDVLDKSGRDYVSQFEGS 60
 Db 1 MKAAVLTAVLFTGSOARHFQWODEPPQSPFWRVKDQATVYVDVLDKSGRDYVSQFEGS 60
 Qy 61 ALGKQLNLKLLDNWDSVTSTFSLKREQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
 Db 61 ALGKQLNLKLLDNWDSVTSTFSLKREQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
 Qy 121 VQPYLDDFQKKWQEMELYKQVEPLRAELQEGARQKLHQLSPLGSEMDRRAHV 180
 Db 121 VQPYLDDFQKKWQEMELYKQVEPLRAELQEGARQKLHQLSPLGSEMDRRAHV 180
 Qy 181 DALRTHLAPYSDELRLQARLALREKNGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
 Db 181 DALRTHLAPYSDELRLQARLALREKNGCGARLAEYHAKATEHLSTLSEKAKPALEDLRQ 240
 Qy 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267
 Db 241 GLLPVLESFKVSFLSALEEYTKKLNTQ 267

RESULT 6
 AAB47620
 ID AAB47620 standard; protein; 267 AA.
 XX
 AC AAB47620;
 XX
 XX 21-JAN-2002 (first entry)
 DT Full length Apo-A1.
 DE
 XX Apolipoprotein; Apo-A1; Apo-A-I fragment T-cell activation inhibitor;
 KW AFT1; monocyte; IL-1; interleukin 1; TNF; tumour necrosis factor;
 KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
 KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;
 KW Parkinson's disease; psoriasis; probe.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 25..194
 FT /label= AFT1
 FT /note= "18 kD N-terminal fragment"
 FT 25..144
 FT /label= AFT1
 FT /note= "13 kD N-terminal fragment"
 FT 44..65
 FT /label= Helical lipid binding domain
 FT 44..65
 FT /label= Amphipathic helix
 FT 66..120

FT /label= Phylogenetically conserved domain
 FT 66..98
 FT /label= Amphipathic helix
 FT 74..111
 FT /note= "Involved in lipoprotein-mediated cholesterol
 FT efflux from monocytes"
 FT 90..111
 FT /note= "Involved in lectin-cholesterol acyltransferase
 FT activity"
 FT 99..143
 FT /label= Hinged domain
 FT 99..120
 FT /label= Major antigenic epitope domain
 FT 99..120
 FT /label= Amphipathic helix
 FT 121..142
 FT /label= Amphipathic helix
 FT 143..164
 FT /label= Amphipathic helix
 FT 149..219
 FT /label= Receptor binding domain
 FT 156..267
 FT /label= AFT1
 FT /note= "13 kD C-terminal fragment"
 FT 165..208
 FT /label= Amphipathic helix
 FT 209..219
 FT /label= Amphipathic helix
 FT 220..241
 FT /label= Helical lipid binding domain
 FT 220..241
 FT /label= Amphipathic helix
 XX
 PN WC200168852-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 13-MAR-2001; 2001WO-US007826.
 XX
 XX 13-MAR-2000; 2000US-0189008P.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Edwards CK, Burger D, Dayer J, Kohno T;
 PI
 XX WPI: 2001-596908/67.
 DR N-PSDB; AAH43623.
 XX
 XX Apo-A-I fragment T-cell activation inhibitor (AFT1) polynucleotides,
 PT useful for treating, diagnosing, ameliorating diseases associated with IL
 PT -1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease and
 PT asthma.
 XX
 PS Claim 1; Fig 1A; 132pp; English.

This sequence shows full length apolipoprotein (Apo-A1). Fragments of Apo
 -A1 may be used as Apo-A-I fragment T-cell activation inhibitors (AFT1).
 These fragments are selected from an 18 kD N-terminal fragment (amino
 acids 25-194), a 13 kD N-terminal fragment (amino acids 25-144) and a 13
 kD C-terminal fragment (amino acids 156-267). The AFT1 polypeptides and
 polynucleotides are useful for regulating T-cell mediated activation of
 monocytes and for treating, diagnosing, ameliorating diseases associated
 with IL-1 and/or TNF activity. The diseases are acute pancreatitis,
 Alzheimer's disease, asthma, cancer, fever, inflammatory bowel disease,
 ischemia, multiple sclerosis, osteoporosis, Parkinson's disease or
 psoriasis. Numerous examples of other diseases are given in the
 specification. The AFT1 nucleic acids are useful as hybridization probes
 in diagnostic assays to test for the presence of an AFT1 or Apo-A-I DNA
 in mammalian tissue or bodily fluid samples

SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 4; Length 267;

Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAVALTLAVLFLTGSQARHFVQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60
DB 1 MKAVALTLAVLFLTGSQARHFVQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60

QY 61 ALGKQLNLKLDNDWSDVSTFSKLEQQLGPVTOEFWDLNLEKETEGRLQEMSKDLEEVKAK 120
DB 61 ALGKQLNLKLDNDWSDVSTFSKLEQQLGPVTOEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180
DB 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALREYTKKLNTQ 267
DB 241 GLLPVLESFKVSFLSALREYTKKLNTQ 267

RESULT 7
AAO15892
ID AAO15892 standard; protein; 267 AA.
AC AAO15892;
XX
XX
XX 30-JAN-2003 (first entry)
XX Human apolipoprotein A-1 (APOA1).
DE Human; gene therapy; single nucleotide polymorphism; SNP;
XX Cytochrome C oxidase subunit VIB; COX6B; high serum cholesterol; GPI-1;
KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
KW Glycosylphosphatidylinositol-1; low serum high density lipoprotein.
XX Homo sapiens.
XX WO200272604-A2.
XX
XX 19-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US006728.
XX
XX 09-MAR-2001; 2001US-00802640.
XX (SEQU-) SEQUENOM INC.
XX Braun A, Bansal A, Kleyn PW;
XX WPI; 2002-750478/81.
XX N-PSDB; ABT13014.
XX
XX Detecting the presence or absence of an allelic variant of a polymorphic
PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
PT to high serum cholesterol, low serum HDL and cardiovascular disease.
XX
XX Disclosure; Page 137-138; 199pp; English.

XX The invention comprises methods of detecting the presence or absence of
CC at least one allelic variant of a polymorphic region of a gene associated
CC with cardiovascular disease. The invention specifically relates to
CC detecting the region of a cytochrome C oxidase subunit VIB (COX6B) gene
CC that is associated with high serum cholesterol, or the region of the N-
CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
CC (GPI-1) gene that is associated with low serum high density lipoprotein
CC (HDL). The methods of the invention are useful for detecting a
CC predisposition to high serum cholesterol, low serum HDL and
CC cardiovascular disease. The methods are also useful for elucidating
CC pathological pathways, developing diagnostic assays and new drug

CC therapies for such disorders. The present amino acid sequence represents
CC a human protein that is associated with high serum cholesterol, low serum
CC HDL and/or cardiovascular disease

XX SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAVALTLAVLFLTGSQARHFVQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60
DB 1 MKAVALTLAVLFLTGSQARHFVQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60

QY 61 ALGKQLNLKLDNDWSDVSTFSKLEQQLGPVTOEFWDLNLEKETEGRLQEMSKDLEEVKAK 120
DB 61 ALGKQLNLKLDNDWSDVSTFSKLEQQLGPVTOEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180
DB 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180

QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALREYTKKLNTQ 267
DB 241 GLLPVLESFKVSFLSALREYTKKLNTQ 267

RESULT 8
ABG97593
ID ABG97593 standard; protein; 267 AA.
AC ABG97593;
XX
XX 17-DEC-2002 (first entry)
XX Human apolipoprotein analogue 1 (Apo A1) protein #15.
DE
XX
XX Apolipoprotein analogue; Apo A; arteriosclerosis; endotoxin removal;
KW angina pectoris; myocardial infarction; arterial stenosis; claudication;
KW carotid stenosis; cerebral arterial stenosis; gene therapy; cholesterol;
KW cardiovascular disease.
XX Homo sapiens.
XX WO200238609-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-DK000739.
XX
XX 10-NOV-2000; 2000DK-00001682.
PR 15-JAN-2001; 2001DK-00000057.
PR 26-JAN-2001; 2001US-0264022P.
XX
XX (PROT-) PROTEOPHARMA APS.
XX
XX Graversen J, Moestrup S;
XX WPI; 2002-527481/56.
XX
XX Novel apolipoprotein construct comprising apolipoprotein A linked to
PT carbohydrate, peptide or protein heterologous group, useful for treating
PT plaque/unstable angina pectoris, myocardial infarction, arterial
PT stenoses.
XX
XX Disclosure; Fig 1; 113pp; English.
XX
XX The invention describes an Apolipoprotein (Apo) construct (I) for use as
CC medicament having general formula apo-A-X, where apo-A is an

CC apolipoprotein component such as apolipoprotein AI, AII or AIV, or its
 CC analogue or variant, and X is heterologous group e.g., amino acid,
 CC peptide, protein, carbohydrate or a nucleic acid, providing that when (I)
 CC consists of exactly two identical, native apolipoproteins these are
 CC linked serially. (I) is useful for preparing a pharmaceutical composition
 CC which further comprises excipients, adjuvants, additives, such as
 CC phospholipids, cholesterol or triglycerides. (I) is useful or treating
 CC and/or preventing arteriosclerosis, for removing endotoxins, for treating
 CC angina pectoris including plaque or unstable angina pectoris, myocardial
 CC infarction, arterial stenoses such as claudication, carotid stenosis,
 CC cerebral arterial stenosis and other cardiovascular diseases. The nucleic
 CC acid (III) encoding (I) is useful for gene therapy, where the DNA sequence
 CC encoding (I) is used for transfection or infection of at least one cell
 CC population comprising macrophages or liver cells. (I) has a half-life of
 CC at least the half-life of native apoA-I, A-II or A-IV, preferably two
 CC times higher or more preferably 10 times higher than the half-life of the
 CC apoA molecules. (I) also has a higher binding affinity to cholesterol
 CC compared to native apoA-I, A-II or A-IV. (I) causes substantially no
 CC immune response in humans. This is the amino acid sequence of a human
 CC apolipoprotein (Apo) analogue fragment
 XX
 SQ

Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 5; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.7e-99;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKAAVLTAVLFLTGSQARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQPEGS 60
 DB 1 MKAAVLTAVLFLTGSQARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQPEGS 60
 QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKOLEEVKAK 120
 DB 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKOLEEVKAK 120
 QY 121 VQPYLDDFQKKWQDEEMELYRQKVPEPLRAELQEGARQKLHELOEKLSPLGEMDRARAHV 180
 DB 121 VQPYLDDFQKKWQDEEMELYRQKVPEPLRAELQEGARQKLHELOEKLSPLGEMDRARAHV 180
 QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 QY 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267
 DB 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

RESULT 9

ABR44031
 ID ABR44031 standard; protein; 267 AA.
 XX
 AC ABR44031;

04-AUG-2003 (first entry)

Human apolipoprotein A-I (ApoA-I) protein.

Apolipoprotein A-I; ApoA-I; cardiant; gene therapy; human;
 cardiovascular disorder.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 178
 FT /label= L178P
 FT /note= "wild-type Leu can be replaced with Pro"

W02003035691-A1.

01-MAY-2003.

25-OCT-2002; 2002WO-CA001615.

XX 26-OCT-2001; 2001US-0335075P.
 PR (XENO-) XENON GENETICS INC.
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA Brownlie AJ, Dube M, Samuels M, Hayden MR;
 PI WPI; 2003-449258/42.
 XX N-PSDB; ACC48172.

DR New Apolipoprotein A-1 mutation, useful for preparing a composition for
 XX treating cardiovascular disorder.
 XX Claim 19; Page 33; 52pp; English.

XX The invention relates to a mutation of the apolipoprotein A-I (ApoA-I)
 CC comprising a leucine to proline variant in position 178. The mutant ApoA-
 CC I polynucleotide is useful for preparing a composition for treating
 CC cardiovascular disorder. The present sequence represents a human ApoA-I
 CC wild-type protein
 XX
 SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 6; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.7e-99;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKAAVLTAVLFLTGSQARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQPEGS 60
 DB 1 MKAAVLTAVLFLTGSQARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQPEGS 60
 QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKOLEEVKAK 120
 DB 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKOLEEVKAK 120
 QY 121 VQPYLDDFQKKWQDEEMELYRQKVPEPLRAELQEGARQKLHELOEKLSPLGEMDRARAHV 180
 DB 121 VQPYLDDFQKKWQDEEMELYRQKVPEPLRAELQEGARQKLHELOEKLSPLGEMDRARAHV 180
 QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
 QY 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267
 DB 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

RESULT 10

ABP57065
 ID ABP57065 standard; protein; 267 AA.
 XX
 AC ABP57065;

14-APR-2003 (first entry)

Human apolipoprotein (APOA1) protein SEQ ID NO:10.

Atherosclerosis; pro-atherogenic inhibitor; antiatherosclerotic;
 macrophage-specific expression element; gene therapy; apolipoprotein;
 APOA1.

Homo sapiens.

W02003002061-A2.

09-JAN-2003.

26-JUN-2002; 2002WO-US020350.

26-JUN-2001; 2001US-00893366.

PA	(UYSA-) UNIV SAN DIEGO STATE FOUND.	XX	Human; apolipoprotein A-I; apo-A-I; T-cell activation inhibitor-like;
XX		KW	AFRI; T-cell-mediated activation; monocyte; interleukin-1beta; IL-1beta;
PI	Davis RA;	KW	tumour necrosis factor alpha; TNF-alpha; gene therapy;
XX		KW	IL-1-mediated disease; acute pancreatitis; Alzheimer's disease; asthma;
DR	WPI; 2003-201457/19.	KW	cancer; diabetes; glomerulonephritis; multiple sclerosis; osteoporosis;
DR	N-PSDB; ABZ59334.	KW	pain; Parkinson's disease; psoriasis; uveitis; TNF-mediated disease;
XX		KW	depression; pancreatitis; periodontal disease; pulmonary fibrosis;
PT	Novel nucleic acid useful for inhibiting or reducing atherosclerosis,	KW	reperfusion injury; rheumatic disease; septic shock;
PT	comprises nucleotide sequence encoding an inhibitor of a pro-atherogenic	KW	systemic lupus erythematosus; thyroiditis; neurotropic; neuroprotective;
PT	molecule operationally linked to a macrophage-specific expression	KW	cystostatic; nephrotropic; analgesic; ophthalmological; antiinflammatory;
XX	element.	KW	vasotrophic; antibacterial; immunosuppressive; dermatological.
PS	Disclosure; Page 95; 99pp; English.	XX	
XX		OS	Homo sapiens.
CC	The present invention describes a nucleic acid (I) comprising a	XX	
CC	nucleotide sequence encoding an inhibitor of a pro-atherogenic molecule	XX	US2002064820-A1.
CC	operationally linked to a macrophage-specific expression element. Also	PN	
CC	described: (1) a vector (II) comprising (I); (2) an embryonic stem cell	XX	30-MAY-2002.
CC	(III) comprising (I); (3) an isolated mammalian cell (IV) comprising (I);	PD	
CC	(4) a recombinant cell (V) comprising a macrophage expressing nucleic	XX	
CC	acid encoding an inhibitor of a pro-atherogenic molecule; (5) a	PF	13-MAR-2001; 2001US-00803918.
CC	transgenic non-human mammal (VI) comprising recombinant cells containing	XX	
CC	a transgenic nucleic acid encoding an inhibitor of a pro-atherogenic	PR	13-MAR-2000; 2000US-0189008P.
CC	molecule; and (6) a non-human mammalian cell (VII) isolated from (VI).	PR	31-MAR-2000; 2000US-0193551P.
CC	(I) has antiatherosclerotic activity and can be used in gene therapy. (I)	XX	(DAYE/) DAYER J.
CC	or (V) can be used for inhibiting or reducing atherosclerosis, by	PA	(BURG/) BURGER D.
CC	administering to an individual (I) or a population of (VI), where the	PA	(KOHN/) KOHNO T.
CC	population of (V) is derived from leukocytes, monocytes, macrophages or	PA	(EDWA/) EDWARDS C K.
CC	stem cells, (V) or (VI) is useful to screen for a drug potentially	XX	
CC	effective for treating atherosclerosis. (V) is useful for identifying a	PI	Dayer J, Burger D, Kohno T, Edwards CK;
CC	compound that reduces susceptibility to developing atherosclerosis. (VI)	XX	
CC	is useful for determining the role of an inhibitor of pro-atherogenic	XX	WPI; 2003-615701/58.
CC	molecule in a particular pathological phenotype or condition of an animal	DR	N-PSDB; ADA61213.
CC	model for atherosclerosis used in drug development. The present sequence	XX	
CC	represents human apolipoprotein (APOA1), which is given in the	PT	New apolipoprotein A-I polypeptide or its related polypeptide termed apo-
CC	exemplification of the present invention	PT	A-I fragment T-cell activation inhibitor-like polypeptide, useful for
XX		PT	treating interleukin-1 or tumor necrosis factor-alpha mediated disease.
XX		XX	
XX		PS	Claim 1; Fig 1A; 56pp; English.
XX		XX	
XX		CC	The invention discloses a apolipoprotein A-I (apo-A-I) polypeptide or its
XX		CC	related polypeptide, apo-A-I fragment T-cell activation inhibitor-like
XX		CC	(AFRI) polypeptide, or a fragment or an allelic or splice variant. Apo-A-
XX		CC	I and its derivatives are used in regulating T-cell-mediated activation
XX		CC	of monocytes. Also disclosed is an antibody produced by immunising an
XX		CC	animal with apo-A-I and a selective binding agent, or its fragment. Apo-A
XX		CC	-I is useful for reducing inflammation, interleukin (IL)-1beta secretion
XX		CC	or tumour necrosis factor (TNF)-alpha secretion in a subject, or for
XX		CC	treating IL-1 or TNF-alpha mediated disease in a subject. The
XX		CC	compositions of the invention are useful for treating (e.g. gene
XX		CC	therapy), preventing or ameliorating a medical condition involving
XX		CC	monocyte activation in a patient, for determining whether a compound
XX		CC	inhibits activity or production of apo-A-I, for detecting or quantifying
XX		CC	the amount of apo-A-I in a sample, for regulating T-cell-mediated
XX		CC	activation of monocytes, to identify a molecule that binds to apo-A-I,
XX		CC	for identifying AFRI receptors, for cloning AFRI receptors, and as an
XX		CC	immunogen to raise antibodies, for treating acute and chronic IL-1-
XX		CC	mediated diseases such as acute pancreatitis, Alzheimer's disease,
XX		CC	asthma, cancer, diabetes, glomerulonephritis, multiple sclerosis,
XX		CC	osteoporosis, pain, Parkinson's disease, psoriasis, uveitis, and acute
XX		CC	and chronic TNF-mediated diseases such as depression, pancreatitis,
XX		CC	periodontal diseases, pulmonary fibrosis, reperfusion injury, rheumatic
XX		CC	diseases, septic shock, systemic lupus erythematosus and thyroiditis.
XX		CC	They are also useful for regulating expression and modulating levels of
XX		CC	apo-A-I, as hybridisation probes in diagnostic assays, for diagnostic
XX		CC	applications, to test for the presence of apo-A-I in cells, for in vivo
XX		CC	imaging and in therapeutics. The sequence presented is the human apo-A-1
XX		CC	protein which comprises an 18K N-terminal or 13K N- or C-terminal
XX		XX	fragments of the apo-A-1 protein.
XX		XX	
XX		XX	Sequence 267 AA;
XX		XX	
XX		XX	Query Match
XX		XX	100.0%; Score 1362; DB 6; Length 267;
XX		XX	Best Local Similarity 100.0%; Pred. No. 3.7e-99;
XX		XX	Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MKAVALTLAVLFLGSGQARHFQQDEPPQSPWDRVKDLATVYVDLKDGRDYVSQEGS 60		
Db	1 MKAVALTLAVLFLGSGQARHFQQDEPPQSPWDRVKDLATVYVDLKDGRDYVSQEGS 60		
Qy	61 ALGQNLNKLDDNDSVTSTSKLREQLGPTQEFWDLNLEKETGLRQEMSKDEEVKAK 120		
Db	61 ALGQNLNKLDDNDSVTSTSKLREQLGPTQEFWDLNLEKETGLRQEMSKDEEVKAK 120		
Qy	121 VQPYLDDFQKKQWEMELYRQKVEPLRAELQEGARQKLHEIQEKLSPLGEEMRDRARAHV 180		
Db	121 VQPYLDDFQKKQWEMELYRQKVEPLRAELQEGARQKLHEIQEKLSPLGEEMRDRARAHV 180		
Qy	181 DALRTHLAPYSDELQRRLAARLEALKENGGRARLAIFYHAKATEHLSTLSEKAKPALEDLRQ 240		
Db	181 DALRTHLAPYSDELQRRLAARLEALKENGGRARLAIFYHAKATEHLSTLSEKAKPALEDLRQ 240		
Qy	241 GLLPVLESFKVSFLSALBEYTKLNTQ 267		
Db	241 GLLPVLESFKVSFLSALBEYTKLNTQ 267		
RESULT 11			
ADA61214			
ID	ADA61214 standard; protein; 267 AA.		
XX			
AC	ADA61214;		
XX			
DT	20-NOV-2003 (first entry)		
XX			
DE	Human apolipoprotein A-1 (apo-A-1).		
			100.0%; Score 1362; DB 6; Length 267;
			Query Match

Best Local Similarity 100.0%; Pred. No. 3.7e-99;		Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MKAAVLTAVLFTGSGARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDVVSQFEGS	60
Db	1	MKAAVLTAVLFTGSGARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDVVSQFEGS	60
QY	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGFPVTOEFWDNLEKETEGRLQEMSKDLEEVKAK	120
Db	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGFPVTOEFWDNLEKETEGRLQEMSKDLEEVKAK	120
QY	121	VQPYLDDFOKKWOEMELRYQKVEPLRAELQEGARQKLHELQKLSPLGEMDRARAHV	180
Db	121	VQPYLDDFOKKWOEMELRYQKVEPLRAELQEGARQKLHELQKLSPLGEMDRARAHV	180
QY	181	DALRTHLAPYSDELQRLARLAKENGCGARLAETHLSTLSEKAKPALEDLRQ	240
Db	181	DALRTHLAPYSDELQRLARLAKENGCGARLAETHLSTLSEKAKPALEDLRQ	240
QY	241	GLLPVLESFKVSFLSALAEYTKKLNQ 267	
Db	241	GLLPVLESFKVSFLSALAEYTKKLNQ 267	
RESULT 12			
ID	ADJ83084		
XX	ADJ83084 standard; protein; 267 AA.		
XX	ADJ83084;		
DT	06-MAY-2004 (first entry)		
XX	Human apolipoprotein A-I precursor protein - SEQ ID 75.		
XX	NOVX; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic;		
KW	antiallergic; antiinflammatory; respiratory; antiarthritic;		
KW	dermatological; antibacterial; cerebroprotective; vasotropic; cardiant;		
KW	haemostatic; hypotensive; hepatotropic; neuroprotective; anorectic;		
KW	neotropic; antitumor; muscular; immunosuppressive; gynaecological;		
KW	antiparotatic; endocrine; ophthalmological; osteopathic;		
KW	antiparkinsonian; anticonvulsant; tranquiliser; analgesic; nephrotropic;		
KW	antiinfertility; antilipaemic; cardiomyopathy; atherosclerosis; diabetes;		
KW	cell signal processing; metabolic pathway; asthma; allergy; emphysema;		
KW	autoimmune; graft-versus-host; arthritis; cancer; stroke; haemophilia;		
KW	obesity; Alzheimer's; pain; chromosome mapping; tissue typing; human;		
XX	apolipoprotein A-I precursor.		
OS	Homo sapiens.		
XX	US2003170630-A1.		
PN	11-SEP-2003.		
PD			
XX	21-DEC-2001; 2001US-00032189.		
XX			
XX	21-DEC-2000; 2000US-0257495P.		
PR	22-DEC-2000; 2000US-0258171P.		
PR	20-FEB-2001; 2001US-0269940P.		
PR	08-MAR-2001; 2001US-0274192P.		
PR	22-MAR-2001; 2001US-0277826P.		
PR	29-MAR-2001; 2001US-0279840P.		
PR	11-APR-2001; 2001US-0282981P.		
PR	13-APR-2001; 2001US-0283656P.		
PR	31-JUL-2001; 2001US-0309247P.		
PR	10-AUG-2001; 2001US-0311754P.		
PR	17-AUG-2001; 2001US-0313331P.		
XX	(ALSO/) ALSOBROOK J P.		
PA	(TCHE/) TCHERNEV V T.		
PA	(LIUX/) LIU X.		
PA	(SPYT/) SPYTEK K A.		
PA	(ZERH/) ZERHUSEN B D.		
PA	(PATT/) PATTURAJAN M.		
PA	(LEPL/) LEPLEY D M.		
PA	(BURG/) BURGESS C E.		
PA	(SHIM/) SHIMKETS R A.		
PA	(GROS/) GROSSE W M.		
PA	(SZEK/) SZEKERES E S.		
PA	(VERN/) VERNET C A M.		
PA	(LILL/) LI L.		
PA	(CASM/) CASMAN S J.		
PA	(BOLD/) BOLDOG F L.		
PA	(GORM/) GORMAN L.		
PA	(GANG/) GANGOLLI E A.		
PA	(FERN/) FERNANDES E R.		
PA	(RIEG/) RIEGER D K.		
PA	(EDIN/) EDINGER S R.		
PA	(GUNT/) GUNTHER E.		
PA	(MILL/) MILLET I.		
PA	(SCIO/) SCORE P.		
PA	(ELLE/) ELLERMAN K.		
PA	(MACD/) MACDOUGALL J R.		
PA	(SMIT/) SMITHSON G.		
XX			
PI	Alsobrook JP, Tchernev VT, Liu X, Spytek KA, Zerhusen BD;		
PI	Patturajan M, Lepley DM, Burgess CE, Shimkets RA, Grosse WM;		
PI	Szekeres ES, Vernet CAM, Li L, Casman SJ, Boldog FL, Gorman L;		
PI	Gangolli EA, Fernandes ER, Rieger DK, Edinger SR, Gunther E;		
PI	Millet I, Sciore P, Ellerman K, Macdougall JR, Smithson G;		
XX	WPI; 2003-898249/82.		
DR			
XX	New NOVX polypeptides and nucleic acid molecules, useful for diagnosing,		
PT	preventing or treating NOVX-associated polypeptide disorder, e.g.		
PT	cardiomyopathy, atherosclerosis, diabetes, cancer, Parkinson's disease or		
PT	asthma.		
XX			
PS	Disclosure; SEQ ID NO 75; 263pp; English.		
XX			
CC	The invention relates to a novel isolated NOVX polypeptide. The		
CC	polypeptide demonstrates cytostatic, antiarteriosclerotic, antidiabetic,		
CC	asthmatic, antiallergic, antiinflammatory, respiratory,		
CC	antiarthritic, dermatological, antibacterial, cerebroprotective,		
CC	vasotropic, cardiant, haemostatic, hypotensive, hepatotropic,		
CC	neuroprotective, anorectic, neotropic, antitumor, antilipaemic,		
CC	immunosuppressive, gynaecological, antiparkinsonian, anticonvulsant,		
CC	ophthalmological, osteopathic, antiparkinsonian, anticonvulsant,		
CC	tranquilliser, analgesic, nephrotropic, antiinfertility and antilipaemic		
CC	activities. The NOVX polypeptide, nucleic acid or antibody of the		
CC	invention may be useful for treating or preventing a NOVX-associated		
CC	disorder, such as cardiomyopathy, atherosclerosis, diabetes or a disorder		
CC	related to cell signal processing and metabolic pathway modulation.		
CC	Furthermore, the NOVX polypeptides may be useful for diagnosing, treating		
CC	or preventing diseases such as asthma, allergies, emphysema, autoimmune		
CC	disease, graft-versus-host disease, arthritis, cancer, stroke,		
CC	haemophilia, obesity, Alzheimer's disease and pain. The nucleic acids may		
CC	be used as hybridisation probes, in chromosome mapping, tissue typing, of		
CC	preventive medicine or pharmacogenomics. The current sequence is that of		
CC	a protein of the invention which is related to human NOVX protein.		
XX			
SQ	Sequence 267 AA;		
Query Match 100.0%; Score 1362; DB 7; Length 267;			
Best Local Similarity 100.0%; Pred. No. 3.7e-99;			
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MKAAVLTAVLFTGSGARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDVVSQFEGS	60
Db	1	MKAAVLTAVLFTGSGARHFQODEPPQSPWDRVKDLATVYVDVLKDSGRDVVSQFEGS	60
QY	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGFPVTOEFWDNLEKETEGRLQEMSKDLEEVKAK	120
Db	61	ALGKQLNLKLLDNWDSVTSTFSKLRQLGFPVTOEFWDNLEKETEGRLQEMSKDLEEVKAK	120
QY	121	VQPYLDDFOKKWOEMELRYQKVEPLRAELQEGARQKLHELQKLSPLGEMDRARAHV	180

Db 121 VQPLDDFQKKQWEMELYRQVEPLRAELQEGARQKLHQLQEKLSPLGEMDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLSEFKVSFLSALEEYTKKLTNQ 267
Db 241 GLLPVLSEFKVSFLSALEEYTKKLTNQ 267

RESULT 13
ADI19752
ID ADI19752 standard; protein; 267 AA.
XX AC ADI19752;
XX DT 22-APR-2004 (first entry)
XX DE Human APOA1 protein.
XX KW Pro-atherogenic; atherosclerosis; therapy; human; apolipoprotein; APOA1;
KW macrophage-specific expression element.
XX OS Homo sapiens.
XX PN US2004001810-A1.
XX PD 01-JAN-2004.
XX PF 26-JUN-2002; 2002US-00186288.
XX PR 26-JUN-2002; 2002US-00186288.
XX PA (DAVI/) DAVIS R A.
XX PI Davis RA;
XX DR WFI; 2004-061641/06.
XX DR N-PSDB; ADI19751.
XX DR GENBANK; XM_006435.
XX PT New nucleic acids encoding an inhibitor of a pro-atherogenic molecule
PT operationally linked to a macrophage-specific expression element, useful
PT for reducing or inhibiting atherosclerosis.
XX PS Disclosure; SEQ ID NO 10; 45pp; English.
XX CC The present invention provides a nucleic acid comprising a nucleotide
CC sequence encoding an inhibitor of a pro-atherogenic molecule
CC operationally linked to a macrophage-specific expression element. The
CC invention is useful for reducing and inhibiting atherosclerosis. The
CC present sequence is human apolipoprotein (APOA1) protein.
XX SQ Sequence 267 AA;
Query Match 100.0%; Score 1362; DB 8; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFTGTSQARHFQWQDEPPQSPWDRVKDLATVYVDLKDGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFTGTSQARHFQWQDEPPQSPWDRVKDLATVYVDLKDGRDYVSQFEGS 60
Qy 61 ALGKQLNKLKLDNWDSTVTSFSLREQLGVPVTOEFWDNLEKETEGRLQKMSKLEEVKAK 120
Db 61 ALGKQLNKLKLDNWDSTVTSFSLREQLGVPVTOEFWDNLEKETEGRLQKMSKLEEVKAK 120
Qy 121 VQPLDDFQKKQWEMELYRQVEPLRAELQEGARQKLHQLQEKLSPLGEMDRARAHV 180
Db 121 VQPLDDFQKKQWEMELYRQVEPLRAELQEGARQKLHQLQEKLSPLGEMDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLSEFKVSFLSALEEYTKKLTNQ 267
Db 241 GLLPVLSEFKVSFLSALEEYTKKLTNQ 267

RESULT 14
ABM81308
ID ABM81308 standard; protein; 267 AA.
XX AC ABM81308;
XX DT 18-NOV-2004 (first entry)
XX DE Tumour-associated antigenic target (TAT) polypeptide PRO36215, SEQ:3377.
XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN WO2004030615-A2.
XX PD 15-APR-2004.
XX PF 29-SEP-2003; 2003WO-US028547.
XX PR 02-OCT-2002; 2002US-0414971P.
XX PA (GETH) GENENTECH INC.
XX PI Wu TD, Zhang Z, Zhou Y;
XX DR WPI; 2004-347921/32.
XX DR N-PSDB; ACN39312.
XX PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX PS Claim 12; SEQ ID NO 3377; 7273pp; English.
XX CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention
SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 8; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFLTGSQARHFQWQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFLTGSQARHFQWQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180

Qy 181 DALRTHLAPYSDELRLORLAARLALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLORLAARLALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALEYTKKLTNQ 267
Db 241 GLLPVLESFKVSFLSALEYTKKLTNQ 267

RESULT 15
ADY75146
ID ADY75146 standard; protein; 267 AA.
XX AC ADY75146;
XX XX
DT 02-JUN-2005 (first entry)
DE Brain tumor marker protein SEQ ID NO 14.
XX
XX KW selectable marker; brain tumor; cytostatic; neoplasm;
XX KW neurological disease; brain tumor marker protein.
XX OS Homo sapiens.
XX
PN WO2005024023-A1.
XX
XX PD 17-MAR-2005.
XX
XX PF 30-APR-2004; 2004WO-JP006345.
XX
XX PR 01-SEP-2003; 2003JP-00309356.
XX
XX PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
XX
XX PI Iwade Y, Hiwasa T, Takiguchi M, Yamaura A;
XX
XX DR WPI; 2005-233288/24.
XX
XX DR N-PSDB; ADY75162.
XX
XX PT New brain tumor marker protein, expressed in brain tumor tissue, such as
XX PT high-malignancy brain tumor, low-malignancy brain tumor, drug-sensitive
XX PT brain tumor or drug-resistant brain tumor, for diagnosing brain tumor.
XX
XX PS Claim 1; SEQ ID NO 14; 115pp; Japanese.
XX
XX CC The invention describes a brain tumor marker protein (I) that is
XX CC expressed in brain tumor tissue, comprising an amino acid sequence chosen
XX CC from 16 fully defined 193-633 amino acid sequences (SEQ ID No: 1-16),
XX CC given in the specification, where each protein is expressed in one or
XX CC more of high-malignancy brain tumor, low-malignancy brain tumor, drug-
XX CC sensitive brain tumor or drug-resistant brain tumor. Also described are:
XX CC an antibody (II) that specifically binds with (I); a diagnostic kit (III)
XX CC comprising (II) and/or labeled (II); a polynucleotide (IV) encoding (I);
XX CC a DNA fragment (V) comprising a portion of contiguous sequence of 16
XX CC fully defined 579-1899 nucleotide sequences (SEQ ID No: 17-32), given in
XX CC the specification; a DNA microarray (VI) comprising (IV) and/or (V); and
XX CC a primer set (VII) for carrying out PCR amplification of SEQ ID No: 17-

CC 32. (IV) Is useful for diagnosing high-malignancy brain tumor, low-
CC malignancy brain tumor, drug-sensitive brain tumor or drug-resistant
CC brain tumor, which involves determining expression level of (IV) in
CC biological sample of the subject, where if the expression level of (IV)
CC is high when compared to healthy person, then the subject is diagnosed to
CC have the above disease. (I) is useful as a diagnostic marker for
CC diagnosing high-malignancy brain tumor, low-malignancy brain tumor, drug-
CC sensitive brain tumor or drug-resistant brain tumor, and for selecting an
CC effective treatment for the diseases. (I) Allows convenient and precise
CC diagnosis of high-malignancy brain tumor, low-malignancy brain tumor,
CC drug-sensitive brain tumor or drug-resistant brain tumor, and selection
CC of effective treatment for the above. This is the amino acid sequence of
CC a brain tumor marker protein.
XX
SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFLTGSQARHFQWQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFLTGSQARHFQWQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWDNLEKETEGRLQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEMDRARAHV 180

Qy 181 DALRTHLAPYSDELRLORLAARLALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLORLAARLALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALEYTKKLTNQ 267
Db 241 GLLPVLESFKVSFLSALEYTKKLTNQ 267

Search completed: March 28, 2006, 20:23:35
Job time : 191 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 20:23:53 ; Search time 41 Seconds
(without alignments)
626.582 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKAVALTLAVLFLTGSQARH.....SPKVSFLSALREYTKLNTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1362	100.0	267	1 LPHUA1	apolipoprotein A-I
2	1306	95.9	267	2 JS0079	apolipoprotein A-I
3	1299	95.4	267	1 A26529	apolipoprotein A-I
4	1161.5	85.3	266	1 LPDGA1	apolipoprotein A-I
5	1100.5	80.8	266	1 LPRB12	apolipoprotein A-I
6	1100	80.8	265	2 A46018	apolipoprotein A-I
7	1093	80.2	265	2 JTO672	apolipoprotein A-I
8	1087.5	79.8	264	2 S31394	apolipoprotein A-I
9	1082	79.4	265	1 LPRB1B	apolipoprotein A-I
10	1082	79.4	265	2 A56858	apolipoprotein A-I
11	974.5	71.5	241	2 A24998	apolipoprotein A-I
12	924	67.8	231	2 JQ0704	apolipoprotein A-I
13	904.5	66.4	264	2 S22420	apolipoprotein A-I
14	898.5	66.0	262	2 JC1237	apolipoprotein A-I
15	849.5	62.4	259	2 A24700	apolipoprotein A-I
16	688.5	50.6	264	1 LPCA1	apolipoprotein A-I
17	663.5	48.7	264	2 JCS456	apolipoprotein A-I
18	644.5	47.3	246	2 A61448	apolipoprotein A-I
19	617.5	45.3	164	2 S21830	apolipoprotein A-I
20	291	21.4	429	2 S29565	apolipoprotein A-I
21	278.5	20.4	396	1 LPHUA4	apolipoprotein A-I
22	267	19.6	391	1 LPTA4	apolipoprotein A-I
23	253	18.6	399	2 C40892	apolipoprotein A-I
24	251	18.4	391	2 B40892	apolipoprotein A-I
25	251	18.4	395	2 A40892	apolipoprotein A-I
26	249.5	18.3	401	2 A47141	apolipoprotein A-I
27	238.5	17.5	394	2 A25281	apolipoprotein A-I
28	225.5	16.6	258	2 JH0472	apolipoprotein A-I
29	209	15.3	311	2 JH0036	apolipoprotein E p

30	198	14.5	312	1 LPRTE	apolipoprotein E p
31	194.5	14.3	1547	2 T28657	blackjack protein,
32	190.5	14.0	317	2 A28792	apolipoprotein E p
33	189.5	13.9	317	2 S03185	apolipoprotein E p
34	188	13.8	317	2 S33450	apolipoprotein E -
35	184	13.5	298	2 S12635	apolipoprotein E p
36	182	13.4	329	2 JCS566	apolipoprotein E p
37	178.5	13.1	291	2 C60940	apolipoprotein E -
38	174.5	12.8	317	1 LPHUE	apolipoprotein E p
39	166.5	12.2	316	2 JCS549	apolipoprotein E p
40	160	11.7	316	2 I45996	apolipoprotein E -
41	160	11.7	316	2 S26478	apolipoprotein E -
42	147	10.8	311	2 A45951	apolipoprotein E p
43	146	10.7	513	2 S08381	keratin, 58K type
44	143.5	10.5	771	1 A33430	h-caldesmon - chic
45	137	10.1	470	2 T23512	hypothetical prote

ALIGNMENTS

RESULT 1

LPHUA1

apolipoprotein A-I precursor [validated] - human

N:Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor
C:Species: Homo sapiens (man)

C>Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 09-Jul-2004

C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; A216197

R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.

DNA 3, 309-317, 1984

A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for human

A:Reference number: A90947; MUID:85026665; PMID:6207999

A:Accession: A90947

A:Molecule type: DNA

A:Residues: 1-267 <SEI>

A:Cross-references: UNIPROT:P02647; UNIPARC:UPI000002C911; GB:X01038; NID:g28769; PIDN:C

A:Accession: B90947

A:Molecule type: mRNA

A:Residues: 1-267 <SE2>

A:Cross-references: UNIPARC:UPI000002C911; GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g

R:Marikides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis, V.I

Bur. J. Biochem. 173, 465-471, 1988

A:Title: Sequence and expression of Tangier apoA-I gene.

A:Reference number: S02373; MUID:86196137; PMID:3129297

A:Accession: S02373

A:Molecule type: DNA

A:Residues: 1-267 <MAK>

A:Cross-references: UNIPARC:UPI000002C911; EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID

R:Shoulders, C.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.

Nucleic Acids Res. 11, 2827-2837, 1983

A:Title: Gene structure of human apolipoprotein A1.

A:Reference number: A93465; MUID:83220822; PMID:6406984

A:Accession: A93465

A:Molecule type: DNA

A:Residues: 1-267 <SHO>

A:Cross-references: UNIPARC:UPI000002C911; GB:J00098; GB:J00100; GB:J00101; G

R:Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.

Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A:Title: Isolation and characterization of the human apolipoprotein A-I gene.

A:Reference number: A21147; MUID:84016011; PMID:6413973

A:Accession: A21147

A:Molecule type: DNA

A:Residues: 1-267 <KAR>

A:Cross-references: UNIPARC:UPI000002C911; GB:J00098; GB:J03222; NID:g178765; PIDN:AA859

R:Sharpe, C.R.; Siddoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.E.

Nucleic Acids Res. 12, 3917-3932, 1984

A:Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundance.

A:Reference number: A93519; MUID:84221405; PMID:6328445

A:Accession: A93519

A:Molecule type: mRNA

A:Residues: 1-267 <SHA>

A:Cross-references: UNIPARC:UPI000002C911; GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g

A;Accession: B93519
A;Molecule type: DNA
A;Residues: 1-24 <SH2>
A;Cross-references: UNIPARC:UPI0000174019
R;Cheung, P.; Chan, L.
Nucleic Acids Res. 11, 3703-3715, 1983
A;Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
A;Reference number: A93472; MUID:83220772; PMID:6304641
A;Accession: A93472
A;Molecule type: mRNA
A;Residues: 1-267 <CHE>
A;Cross-references: UNIPARC:UPI000002C911; GB:J00099; GB:J00100; GB:J00101; GB:J00102
R;Law, S.W.; Brewer Jr., H.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
A;Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
A;Reference number: A94010; MUID:84119464; PMID:6198645
A;Accession: A94010
A;Molecule type: mRNA
A;Residues: 1-267 <LAW>
A;Cross-references: UNIPARC:UPI000002C911; GB:J00099; GB:J00100; GB:J00101; GB:J00102
R;Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
A;Title: Intracellular and extracellular processing of human apolipoprotein A-I: secretory pathway
A;Reference number: A21118; MUID:83195100; PMID:6405383
A;Accession: A21118
A;Molecule type: mRNA
A;Residues: 1-24 <ZAN>
A;Cross-references: UNIPARC:UPI0000174019
R;Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Ronan, R.; Law, S.; Light, J.A.
Biochem. Biophys. Res. Commun. 113, 626-632, 1983
A;Title: Human plasma preapo-A-I: isolation and amino-terminal sequence.
A;Reference number: A90112; MUID:83258553; PMID:6409108
A;Accession: A90112
A;Molecule type: protein
A;Residues: 19-27 <BRE>
R;Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Ronan, R.; Houser, A.; Bronzert, T.J.
Biochem. Biophys. Res. Commun. 80, 623-630, 1978
A;Title: The amino acid sequence of human ApoA-I, an apolipoprotein isolated from high density lipoproteins
A;Reference number: A90209; MUID:78123731; PMID:204308
A;Accession: A90209
A;Molecule type: protein
A;Residues: 25-57, 'Q', '59-169, 'QQ', '172-267 <BR2>
A;Cross-references: UNIPARC:UPI0000174018
R;Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
J. Clin. Invest. 82, 803-807, 1988
A;Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I)
A;Reference number: A30516; MUID:88331387; PMID:3047170
A;Accession: A30516
A;Molecule type: protein
A;Residues: 25-56 <YUI>
A;Cross-references: UNIPARC:UPI000017401C
R;Nichols, W.C.; Dwulet, F.E.; Liepnieks, J.; Benson, M.D.
Biochem. Biophys. Res. Commun. 156, 762-768, 1988
A;Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
A;Reference number: A31582; MUID:89050104; PMID:3142462
A;Accession: A31582
A;Molecule type: protein
A;Residues: 25-49, 'R', '51-85, 'D', '87-107 <NIC>
A;Cross-references: UNIPARC:UPI000017401D
A;Note: variant sequence from patient with familial amyloidotic polyneuropathy type III
R;Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.
J. Biol. Chem. 264, 16853-16857, 1989
A;Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
A;Reference number: A34409; MUID:89380318; PMID:2506184
A;Accession: A34409
A;Molecule type: protein
A;Residues: 25-48 <MAN>
A;Cross-references: UNIPARC:UPI000017401E
R;Stoffel, W.; Binczek, E.
Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
A;Title: Structural requirements of human preapoA-I for translocation and secretion
A;Reference number: S02737; MUID:89149957; PMID:3228490

A;Accession: S02737
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-6, 'AV', '9, 'LV', '12-29 <STO>
A;Cross-references: UNIPARC:UPI000017401F
A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by sequencing
R;Stoffel, W.; Binczek, E.
Biol. Chem. Hoppe-Seyler 372, 481-488, 1991
A;Title: Transient expression of wild type and mutant human apolipoprotein AI in COS cells
A;Reference number: S16197; MUID:92029676; PMID:1930731
A;Contents: annotation; extension of studies in reference S02737
R;Stoffel, W.; Kruger, E.; Deutzmann, R.
Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1993
A;Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processing
A;Reference number: A19913; MUID:83236195; PMID:6407957
A;Accession: B19913
A;Molecule type: protein
A;Residues: 1-6, 'X', '8-13, 'XX', '17-18, 'XX', '21, 'X', '23-25, 'X', '27-29 <ST2>
A;Cross-references: UNIPARC:UPI0000174020
R;Ehnhorn, C.; Bozas, S.E.; Tenkannen, H.; Kirsbaum, L.; Metso, J.; Murphy, B.; Walker, J.
Biochim. Biophys. Acta 1086, 255-260, 1991
A;Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein of liver
A;Reference number: A56815; MUID:92075698; PMID:1742316
A;Accession: A56815
A;Molecule type: protein
A;Residues: 25-31, 'P', '33 <EHN>
A;Cross-references: UNIPARC:UPI000006D30A
A;Experimental source: serum
A;Note: 32-Trp was also found
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
A;Reference number: A54223; MUID:94162201; PMID:8117655
A;Accession: A54223
A;Molecule type: protein
A;Residues: 25-39 <KUN>
A;Cross-references: UNIPARC:UPI0000174021
R;Mogulievsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.; He
DNA 8, 429-436, 1989
A;Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: purification and characterization
A;Reference number: I39476; MUID:89377481; PMID:2673706
A;Accession: I39476
A;Molecule type: mRNA
A;Residues: 19-267 <RES>
A;Cross-references: UNIPARC:UPI0000000473; GB:M29068; NID:9178774; PIDN:AAA51747.1; PIDN:AAA51747.2
R;Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
J. Biol. Chem. 263, 18530-18536, 1988
A;Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the 5' flanking region
A;Reference number: I39475; MUID:89054040; PMID:3142880
A;Accession: I39475
A;Molecule type: DNA
A;Residues: 1-14 <RE2>
A;Cross-references: UNIPARC:UPI00000000391; GB:J04066; NID:9178763; PIDN:AAA51746.1; PIDN:AAA51746.2
R;Breslow, J.L.
Annu. Rev. Biochem. 54, 699-727, 1985
A;Title: Human apolipoprotein molecular biology and genetic variation.
A;Reference number: A9042; MUID:85278004; PMID:3896129
A;Contents: annotation; review of sequences, variants and gene location
R;Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.
J. Biol. Chem. 263, 3911-3914, 1986
A;Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acylation
A;Reference number: A92577; MUID:86140194; PMID:3005308
A;Contents: annotation; acylation with palmitate
A;Note: an undetermined serine or threonine is acylated by fatty acid; the acylating fatty acid is palmitic
R;Law, S.W.; Brewer, H.B.
J. Biol. Chem. 260, 12810-12814, 1985
A;Title: Tangier disease: The complete mRNA sequence encoding for preapoA-I.
A;Reference number: I55236; MUID:86008382; PMID:2995392
A;Accession: I55236
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-143, 'D', '145-267 <RE3>

A;Cross-references: UNIPARC:UPI0000052BCB; GB:M11791; NID:g178776; PIDN:AAA35545.1; PID:
C;Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine.
Osteins (HDL) in plasma.

C;Genetics:

A;Gene: GDB:APOA1

A;Cross-references: GDB:119684; OMIM:107680

Query Match 100.0%; Score 1362; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 5.2e-70;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAALVTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFEGS 60

DB 1 MKAALVTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFEGS 60

QY 61 ALGKQLNLKLDNDWDSVTSTFSKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLSEVAK 120

DB 61 ALGKQLNLKLDNDWDSVTSTFSKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLSEVAK 120

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGSEMRDRARAHV 180

DB 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGSEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQ 240

DB 181 DALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSLSALEBYTKKLNQ 267

DB 241 GLLPVLESFKVSLSALEBYTKKLNQ 267

RESULT 2

JS0079

apolipoprotein A-I precursor - baboon

C;Species: Papio sp. (baboon)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Jun-1997

C;Accession: JS0079

R;Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; Vandenberg, J.L.

Gene 74, 483-490, 1988

A;Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and id

A;Reference number: JS0079; MUID:89232739; PMID:2907746

A;Accession: JS0079

A;Molecule type: mRNA

A;Residues: 1-267 <HIX>

A;Cross-references: UNIPARC:UPI0000052BCC

A;Experimental source: liver

C;Comment: This protein is the principal protein component of high density lipoprotein p

C;Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase co

C;Comment: This protein contains a region of repeated amino acids which form amphipathic

C;Genetics:

A;Gene: apoA1

C;Superfamily: apolipoprotein A-I

C;Keywords: HDL; lipid binding; lipoprotein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-267/Product: apolipoprotein A-I #status predicted <LAI>

F;123-144,145-166,167-188,189-210,211-232,233-254/Region: tandem repeats

Query Match 95.9%; Score 1306; DB 2; Length 267;
Best Local Similarity 95.1%; Pred. No. 7.3e-67;
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKAALVTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFEGS 60

DB 1 MKAALVTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFEGS 60

QY 61 ALGKQLNLKLDNDWDSVTSTFSKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLSEVAK 120

DB 61 ALGKQLNLKLDNDWDSVTSTFSKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLSEVAK 120

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGSEMRDRARAHV 180

DB 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGSEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQ 240

DB 181 DALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSLSALEBYTKKLNQ 267

DB 241 GLLPVLESFKVSLSALEBYTKKLNQ 267

RESULT 3

A26529

apolipoprotein A-I precursor - crab-eating macaque

C;Species: Macaca fascicularis (crab-eating macaque)

C;Date: 30-Sep-1989 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Accession: A26529; A26627; S23135; A57766

R;Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marotti, K.R.

Gene 49, 103-110, 1986

A;Title: The primary structure of cynomolgus monkey apolipoprotein A-1 deduced from the

A;Reference number: A26529; MUID:87191989; PMID:3106152

A;Accession: A26529

A;Molecule type: mRNA

A;Residues: 1-267 <POL>

C;Cross-references: UNIPROT:P15568; UNIPARC:UPI0000052BCD; GB:M15411; NID:g342074; PIDN:

R;Herbert, P.N.; Bauserman, L.L.; Lynch, K.M.; Saritelli, A.L.; Kantor, M.A.; Nicolosi,

Biochemistry 26, 1457-1463, 1987

A;Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (cyn

A;Reference number: A26627; MUID:87185451; PMID:3105581

A;Accession: A26627

A;Molecule type: protein

A;Residues: 25-48 <HER>

A;Cross-references: UNIPARC:UPI0000174022

R;Murray, R.W.; Marotti, K.R.

Biochim. Biophys. Acta 1131, 207-210, 1992

A;Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and corres

A;Reference number: S23135; MUID:92305062; PMID:1610902

A;Accession: S23135

A;Molecule type: DNA

A;Residues: 1-12, 'L', '14-267 <MUR>

A;Cross-references: UNIPARC:UPI0000052BCC; GB:M83244; NID:g342070; PIDN:AAA36832.1; PID

R;Sorci-Thomas, M.; Kearns, M.W.

J. Biol. Chem. 266, 18045-18050, 1991

A;Title: Transcriptional regulation of the apolipoprotein A-I gene.

A;Reference number: A57766; MUID:92011532; PMID:1917942

A;Accession: A57766

A;Molecule type: DNA

A;Residues: 1-10 <RES>

A;Cross-references: UNIPARC:UPI00000004AD; GB:M69223; NID:g342066; PIDN:AAA36831.1; PID:

C;Comment: The precursor is synthesized in the liver and small intestine. The propeptide

C;Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins (HD

y promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin

C;Genetics:

A;Introns: 15/1; 67/2

C;Superfamily: apolipoprotein A-I

C;Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repe

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-24/Domain: propeptide #status predicted <PPT>

F;25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 95.4%; Score 1299; DB 1; Length 267;
Best Local Similarity 94.8%; Pred. No. 1.8e-66;
Matches 253; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKAALVTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFEGS 60

DB 1 MKAALVTLAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFEGS 60

QY 61 ALGKQLNLKLDNDWDSVTSTFSKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLSEVAK 120

DB 61 ALGKQLNLKLDNDWDSVTSTFSKLRQLGPVTQEFWDLNLEKETEGRLQEMSKDLSEVAK 120

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGSEMRDRARAHV 180

DB 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGSEMRDRARAHV 180

Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELHEGTRQKQLHELHEKLSPLGEVBRDRARAHV 180

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGGRARLAETHYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELQRLAARLEALKENGGRARLAETHYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALBEYTKKLNQ 267

Db 241 GLLPVLESFKVSFLSALBEYTKKLNQ 267

RESULT 4

LPDGA1

apolipoprotein A-I precursor - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 17-Dec-1982 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: A60940; A03092; A61418

R:Lu, C.C.; Li, W.H.; Chan, L.

J. Lipid Res. 30, 1735-1746, 1989

A:Title: Structure and expression of dog apolipoprotein A-I, B, and C-I mRNAs: implications for the evolution of the apolipoprotein A-I gene

A:Reference number: A60940; MUID:90132271; PMID:2515239

A:Accession: A60940

A:Molecule type: mRNA

A:Residues: 1-266 <LUO>

A:Cross-references: UNIPROT:P02648; UNIPARC:UPI0000125BD7

R:Chung, H.; Randalph, A.; Reardon, I.; Heinrikson, R.L.

J. Biol. Chem. 257, 2961-2967, 1982

A:Title: The covalent structure of apolipoprotein A-I from canine high density lipoproteins

A:Reference number: A03092; MUID:82142425; PMID:6801039

A:Accession: A03092

A:Molecule type: protein

A:Residues: 25-167, 'G', 169-201, 'Q', 203-234, 'Q', 236-266 <CHU>

A:Cross-references: UNIPARC:UPI0000174023

R:Nakai, T.; Whayne, T.F.; Tang, J.

FEBS Lett. 64, 409-411, 1976

A:Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.

A:Reference number: A61418; MUID:76210910; PMID:179887

A:Accession: A61418

A:Molecule type: protein

A:Residues: 25-56, 'Z', 161-262, 'A' <NAK>

A:Cross-references: UNIPARC:UPI0000174024; UNIPARC:UPI0000174025

C:Superfamily: apolipoprotein A-I

C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; lipoproteins

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-24/Domain: propeptide #status predicted <PRO>

F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 85.3%; Score 1161.5; DB 1; Length 266;

Best Local Similarity 85.0%; Pred. No. 9.9e-59;

Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDLVKDSGRDYVSQFEGS 60

Db 1 MKAALLTAVLFLTGSQARHFQQDE-PQSPWDRVKDLATVYVDLVKDSGRDYVAQFEAS 59

Qy 61 ALGKQLNLKLLDNWDSVTSFKLREQLGPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAK 120

Db 60 ALGKQLNLKLLDNWDSVTSFKLREQLGPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAK 119

Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELHEGTRQKQLHELHEKLSPLGEVBRDRARAHV 180

Db 121 DALRTHLAPYSDELQRLAARLEALKENGGRARLAETHYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALBEYTKKLNQ 267

Db 241 GLLPVLESFKVSFLSALBEYTKKLNQ 266

RESULT 5

LPB1Z

apolipoprotein A-I precursor (clone 22ap AI) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C:Accession: S06064

R:Paraskevopoulou, T.B.; Kritis, A.; Zannis, V.

submitted to the EMBL Data Library, July 1989

A:Reference number: S06064

A:Accession: S06064

A:Molecule type: mRNA

A:Residues: 1-266 <PAR>

A:Cross-references: UNIPROT:P09809; UNIPARC:UPI0000125BDC; EMBL:X15908; NID:g1457; PIDN:

C:Comment: This protein is synthesized in the small intestine.

C:Comment: This protein is a major component of the high density lipoproteins in plasma

C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repeat

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-24/Domain: propeptide #status predicted <PRO>

F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 80.8%; Score 1100.5; DB 1; Length 266;

Best Local Similarity 80.1%; Pred. No. 2.7e-55;

Matches 214; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDLVKDSGRDYVSQFEGS 60

Db 1 MKAAVLTAVLFLTGSQARHFQQRDE-PRSSWDKIKDFATVYVDLVKDSGREYVAQFEAS 59

Qy 61 ALGKQLNLKLLDNWDSVTSFKLREQLGPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAK 120

Db 60 AFGKQLNLKLLDNWDSVTSFKLREQLGPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAK 119

Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELHEGTRQKQLHELHEKLSPLGEVBRDRARAHV 180

Db 121 DALRTHLAPYSDELQRLAARLEALKENGGRARLAETHYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALBEYTKKLNQ 267

Db 240 GLLPVLESFKVSFLSALBEYTKKLNQ 266

RESULT 6

A46018

apolipoprotein AI - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A46018

R:Birchbauer, A.; Knipping, G.; Juritsch, B.; Aschauer, H.; Zechner, R.

Genomics 15, 643-652, 1993

A:Title: Characterization of the apolipoprotein AI and CIII genes in the domestic pig.

A:Reference number: A46018; MUID:93224154; PMID:8468059

A:Accession: A46018

A:Status: preliminary

A:Molecule type: DNA; protein

A:Residues: 1-265 <BIR>

A:Cross-references: UNIPROT:P18648; UNIPARC:UPI000016C688; GB:L00626; NID:g164358; PIDN:

A:Note: sequence extracted from NCBI backbone (NCBIN:129509, NCBIP:129511)

C:Superfamily: apolipoprotein A-I

Query Match 80.8%; Score 1100; DB 2; Length 265;

Best Local Similarity 80.9%; Pred. No. 2.9e-55;

Matches 216; Conservative 19; Mismatches 30; Indels 2; Gaps 2;

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDLVKDSGRDYVSQFEGS 60

Db 1 MKAAVLTAVLFLTGSQARHFQQDD-PQSPWDRVKDFATVYVDLVKDSGREYVAQFEAS 59

Qy 61 ALGKQLNLKLLDNWDSVTSFKLREQLGPVTOEFWDLNLEKETEGLRQEMSKDLEEVKAK 120

Db 60 ALGKHLNKLKLDNWDLSGTTFTKVRQQLGPVTQEFWMDNLEKETEALRQEMSKDLEEVKK 119
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLQELQKSLPGLGEMRDRARAHV 180
Db 120 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLQELQKSLPGLGEMRDRARAHV 179
Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 EALRQQLAPYSDDLQQRWAARFEALKEGGS-LASYQAKQEQALKALGEKAKPALEDLRQ 238
Qy 241 GLLPVLESFKVSFLSALAEYTKKLTNQ 267
Db 239 GLLPVLENLKVSIILAAIDEASKKLNQAQ 265

RESULT 7
JT0672
apolipoprotein A-I - pig
N:Alternate names: apo-A-I
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: JT0672; FN0471; A05311
R:Trieu, V.N.; Patel, B.; Zhan, R.; Black, D.D.
Gene 134, 267-270, 1993
A:Title: Sequence of the porcine apoA-I gene.
A:Reference number: JT0672; MUID:94085789; PMID:7916724
A:Accession: JT0672
A:Molecule type: DNA
A:Residues: 1-265 <TRI>
A:CROSS-references: UNIPROT:P18648; UNIPARC:UPI000017779E; EMBL:Z14124; NID:g1893
A:Note: this translation is not annotated in Genbank entry SSAPOAIG, release 111.0; the
R:Trieu, V.N.; Hasler-Rapacz, J.; Rapacz, J.; Black, D.D.
Gene 123, 173-179, 1993
A:Title: Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs.
A:Reference number: FN0471; MUID:93154581; PMID:8428656
A:Accession: FN0471
A:Molecule type: mRNA
A:Residues: 105-265 <TR2>
A:CROSS-references: UNIPARC:UPI000017779F
A:Experimental source: liver
R:Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
Biochemistry 15, 1928-1933, 1976
A:Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocyte
A:Reference number: A90395; MUID:76184721; PMID:178359
A:Accession: A05311
A:Molecule type: protein
A:Residues: 25-34 <MAH>
A:CROSS-references: UNIPARC:UPI00001777A0
C:Comment: This protein is the major apolipoprotein of high-density lipoprotein and serves
C:Genetics:
A:Gene: apoA-I
A:Introns: 15/1, 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; lip
P:99/Region: ochre stop codon

Qy 1 MKAAVLTAVLFLTGSQARHFHQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGS 60
Db 1 MKAVVLTAVLFLTGSQARHFHQDD-PPSPWDRVKDFATVYVDAIKDSGRDYVAQFEAS 59
Qy 61 ALGKLNKLKLDNWDVSTSTFSKLREQLGPVTQEFWMDNLEKETEGLRQEMSKDLEEVKAK 120
Db 60 ALGKHLNKLKLDNWDLSGTTFTKVRQQLGPVTQEFWMDNLEKETEALRQEMSKDLEEVKK 119
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLQELQKSLPGLGEMRDRARAHV 180
Db 120 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLQELQKSLPGLGEMRDRARAHV 178
Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 179 AALRQHVAPYSDDLQQRWAARFEALKE-GGUSLASYQAKQEQALKALGEKAKPALEDLRQ 237
Qy 241 GLLPVLESFKVSFLSALAEYTKKLTNQ 267
Db 238 GLLPVLENLKVSIILAAIDEASKKLNQAQ 264

RESULT 9
LPRB1B
apolipoprotein A-I precursor (clone pRBA-502) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C:Accession: S00230; S20557
R:Pan, T.C.; Hao, Q.L.; Yamin, T.T.; Dai, P.H.; Chen, B.S.; Chen, S.L.; Kroon, P.A.; Cha
Eur. J. Biochem. 170, 99-104, 1987
A:Title: Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein A-
A:Reference number: S00230; MUID:88082866; PMID:3121329
A:Accession: S00230
A:Molecule type: mRNA
A:Residues: 1-265 <PAN>
A:CROSS-references: UNIPARC:UPI000016C53A; EMBL:X06658; NID:g1461; PIDN:CAA29857.1; PID:
A:Note: the authors translated the codon AGC for residue 174 as Arg
A:Accession: S20557
A:Molecule type: DNA
A:Residues: 1-17, 'R', '19-44, 'I', '46-122, 'Y', '124-146, 'V', '148-265 <PAN2>
A:CROSS-references: UNIPARC:UPI000016C539; EMBL:X06659; NID:g1459; PIDN:CAA29858.1; PID:
C:Comment: This protein is synthesized in the small intestine.
C:Comment: This protein is a major component of the high density lipoproteins in plasma.
C:Genetics:
A:Introns: 15/1, 66/2

Db 180 EALRQHVAPYSDDLQQRWAARFEALKEGGS-LASYQAKQEQALKALGEKAKPALEDLRQ 238
Qy 241 GLLPVLESFKVSFLSALAEYTKKLTNQ 267
Db 239 GLLPVLENLKVSIILAAIDEASKKLNQAQ 265

RESULT 8
S31394
apolipoprotein A-I - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31394
R:Moehel, B.; Flach, R.; Weiss, B.; Weiler-Guettler, H.; Frey, A.; Zinke, H.; Gassen, H.
submitted to the EMBL Data Library, November 1992
A:Description: Genomic organization of the porcine apolipoprotein A1 gene and study of g
A:Reference number: S31394
A:Accession: S31394
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <MOE>
A:CROSS-references: UNIPROT:P18648; UNIPARC:UPI000016C68A; EMBL:X69477; NID:g1889; PIDN:
C:Superfamily: apolipoprotein A-I

Query Match 79.8%; Score 1087.5; DB 2; Length 264;
Best Local Similarity 80.9%; Pred. No. 1.4e-54;
Matches 216; Conservative 18; Mismatches 30; Indels 3; Gaps 3;

Qy 1 MKAAVLTAVLFLTGSQARHFHQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGS 60
Db 1 MKAVVLTAVLFLTGSQARHFHQDD-PPSPWDRVKDFATVYVDAIKDSGRDYVAQFEAS 59
Qy 61 ALGKLNKLKLDNWDVSTSTFSKLREQLGPVTQEFWMDNLEKETEGLRQEMSKDLEEVKAK 120
Db 60 ALGKHLNKLKLDNWDLSGTTFTKVRQQLGPVTQEFWMDNLEKETEALRQEMSKDLEEVKK 119
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLQELQKSLPGLGEMRDRARAHV 180
Db 120 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHLQELQKSLPGLGEMRDRARAHV 178
Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 179 AALRQHVAPYSDDLQQRWAARFEALKE-GGUSLASYQAKQEQALKALGEKAKPALEDLRQ 237
Qy 241 GLLPVLESFKVSFLSALAEYTKKLTNQ 267
Db 238 GLLPVLENLKVSIILAAIDEASKKLNQAQ 264

A>Title: Synthesis of apolipoprotein A-1 in pig brain microvascular endothelial cells.
A:Reference number: JQ0704; MUID:90132667; PMID:2105375
A:Accession: JQ0704
A:Molecule type: mRNA
A:Residues: 1-231 <WEI>
A:Cross-references: UNIPARC:UPI0000177799
A>Note: the authors translated the codon CAG for residue 124 as His and GAC for residue 125
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein; pl

Query Match 67.8%; Score 924; DB 2; Length 231;
Best Local Similarity 79.0%; Pred. No. 2e-45;
Matches 184; Conservative 18; Mismatches 29; Indels 2; Gaps 2;

QY 35 VKDLATVYVULKDSGRDYSQFEGSALGKQLNLKLLDNWDSVTSTFKLRQLGPTQOE 94
DB 1 VKDFATVYVDAIKDSGRDYVAQFEASALGKHLNLKLLDNWDSIGSTFTKVRQLGPTQOE 60

QY 95 FWNLEKETEGURQMSKDLREVKAKVQPYLDDFKKKQEMELYRQKVEPLRAELQSGA 154
DB 61 FWNLEKETEARQMSKDLREVKKKVQPYLDDFKKKQEMELYRQKM-PLGAEFRGA 119

QY 155 RQKHELOEKLSPLEGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGGA 214
DB 120 RQKVELQEKSLAEELDRLARAHVAALRQHVAYSDDLQRMARFEALKE-GGDSIA 178

QY 215 EYHAKATEHLSTLSEKAKPALEDLQGLLPVLESFKVSFLSALREYTKKLNQ 267
DB 179 EYQAKAQEQLKALGEKAKPALEDLQGLLPVLENLKVSLAIDAESKKLNQ 231

RESULT 13
S22420
apolipoprotein A-I precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
A:Accession: S22420; S22421; A4364
R:Stoffel, W.; Mueller, R.; Sinczek, E.; Hofmann, K.
Biol. Chem. Hoppe-Seyler 373, 187-193, 1992
A>Title: Mouse apolipoprotein AI. cDNA-derived primary structure, gene organisation and
A:Reference number: S22420; MUID:92281682; PMID:1596360
A:Accession: S22420
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPROT:Q00623; UNIPARC:UPI0000001913; EMBL:X64262; NID:g50014; PIDN
A:Accession: S22421
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <ST2>
A:Cross-references: UNIPARC:UPI0000001913; EMBL:X64263; NID:g50020; PIDN:CAA45561.1; PID
R:Januzzi, J.L.; Azrolan, N.; O'Connell, A.; Aalto-Setälä, K.; Breslow, J.L.
Genomics 14, 1081-1088, 1992
A>Title: Characterization of the mouse apolipoprotein Apoa-1/apoc-3 gene locus: genomic,
A:Reference number: A44364; MUID:93122774; PMID:1478650
A:Accession: A44364
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-264 <JAN>
A:Cross-references: UNIPARC:UPI0000001913
A>Note: sequence extracted from NCBI backbone (NCBIN:122400, NCBI:P:122407)
C:Genetics:
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I

Query Match 66.4%; Score 904.5; DB 2; Length 264;
Best Local Similarity 65.2%; Pred. No. 2.9e-44;
Matches 174; Conservative 41; Mismatches 49; Indels 3; Gaps 2;

QY 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVVLKDSGRDYSQFEGS 60
DB 1 MKAVVLAVALVFLTGSQARHFQQDE-PQSQWDKVDKDFANYVYDAVKDSGRDYSQFESS 59

RESULT 15
A24700
apolipoprotein A-I precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
A:Accession: A24700; S00298; A05314
R:Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A>Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A

Query Match 66.4%; Score 904.5; DB 2; Length 264;
Best Local Similarity 65.2%; Pred. No. 2.9e-44;
Matches 174; Conservative 41; Mismatches 49; Indels 3; Gaps 2;

QY 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVVLKDSGRDYSQFEGS 60
DB 1 MKAVVLAVALVFLTGSQARHFQQDE-PQSQWDKVDKDFANYVYDAVKDSGRDYSQFESS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFKLRQLGPTQOEFDWNLKEKETEGLRQMSKDLREVKAK 120
DB 60 SLGQQLNLNLLENWDTTGSTVSQLERLGLPUTRDFWNLKEKETEGLRQMSKDLREVKAK 119

QY 121 VQPYLDDFKKKQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEGEEMDRARAHV 180
DB 120 VQPYLDFEQKKVEDVELYRQKVAPLGAELQESARQKLQELQGRSLSPAVERFRDRMRTHV 179

QY 181 DALRTHLAPYSDELQRLAARLEALKENGGAARLAIYHAKATEHLSTLSEKAKPALEDLQ 240
DB 180 DSLRTQLAPHSEQRMSLAQRLAEKSN--PTLNEYTHTRAKTHLTKLGEKARPALEDLRH 237

QY 241 GLLPVLESFKVSFLSALREYTKKLNQ 267
DB 238 SLMPWLETLTAKAQSVIDKASETLTAQ 264

RESULT 14
JC1237
apolipoprotein A-I precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 31-Dec-1993
A:Accession: JC1237
R:Boyle, T.P.; Marotti, K.R.
Gene 117, 243-247, 1992
A>Title: Structure of the murine gene encoding apolipoprotein A-I.
A:Reference number: JC1237; MUID:92347700; PMID:1639271
A:Accession: JC1237
A:Molecule type: DNA
A:Residues: 1-262 <BOY>
A:Cross-references: UNIPARC:UPI0000177797; GB:M77801
C:Genetics:
A:Gene: ApoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipop
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-262/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 66.0%; Score 998.5; DB 2; Length 262;
Best Local Similarity 67.1%; Pred. No. 6.2e-44;
Matches 173; Conservative 37; Mismatches 45; Indels 3; Gaps 2;

QY 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVVLKDSGRDYSQFEGS 60
DB 1 MKAVVLAVALVFLTGSQARHFQQDE-PQSQWDKVDKDFANYVYDAVKDSGRDYSQFESS 59

QY 61 ALGKQLNLKLLDNWDSVTSTFKLRQLGPTQOEFDWNLKEKETEGLRQMSKDLREVKAK 120
DB 60 SLGQQLNLNLLENWDTTGSTVSQLERLGLPUTRDFWNLKEKETEGLRQMSKDLREVKAK 119

QY 121 VQPYLDDFKKKQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEGEEMDRARAHV 180
DB 120 VQPYLDFEQKKVEDVELYRQKVAPLGAELQESARQKLQELQGRSLSPAVERFRDRMRTHV 179

QY 181 DALRTHLAPYSDELQRLAARLEALKENGGAARLAIYHAKATEHLSTLSEKAKPALEDLQ 240
DB 180 DSLRTQLAPHSEQRMSLAQRLAEKSN--PTLNEYTHTRAKTHLTKLGEKARPALEDLRH 237

QY 241 GLLPVLESFKVSFLSALREYTKKLNQ 258
DB 238 SLMPWLETLTAKAQSVIDKASETLTAQ 255

apolipoprotein A-I precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
A:Accession: A24700; S00298; A05314
R:Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A>Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A

Search completed: March 28, 2006, 20:28:17
Job time : 42 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 20:39:08 ; Search time 163 Seconds
(without alignments)
684.420 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKAAVLTAVLFLTGSQARH.....SFKVSFLSALREYTKLNTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	267	3 US-09-803-918A-2	Sequence 2, Appli
2	1362	100.0	267	3 US-09-803-918A-2	Sequence 15, Appl
3	1362	100.0	267	3 US-09-803-918A-2	Sequence 30, Appl
4	1362	100.0	267	4 US-10-032-189-75	Sequence 75, Appl
5	1362	100.0	267	4 US-10-032-189-75	Sequence 260, App
6	1362	100.0	267	4 US-10-032-189-75	Sequence 30, Appl
7	1362	100.0	267	4 US-10-032-189-75	Sequence 10, Appl
8	1362	100.0	267	4 US-10-032-189-75	Sequence 219, App
9	1362	100.0	267	4 US-10-032-189-75	Sequence 260, App
10	1362	100.0	267	5 US-10-032-189-75	Sequence 260, App
11	1362	100.0	267	5 US-10-032-189-75	Sequence 2, Appli
12	1362	100.0	267	6 US-11-017-059-15	Sequence 15, Appl
13	1362	100.0	267	6 US-11-017-059-15	Sequence 15, Appl
14	1362	100.0	267	6 US-11-017-059-15	Sequence 15, Appl
15	1362	100.0	275	5 US-10-852-705A-4	Sequence 4, Appli
16	1359	99.8	267	4 US-10-032-189-74	Sequence 74, Appl
17	1359	99.8	267	4 US-10-032-189-74	Sequence 253, App
18	1346	98.8	267	3 US-09-919-039-27	Sequence 27, Appl
19	1306	95.9	267	3 US-09-987-107-16	Sequence 16, Appl
20	1306	95.9	267	4 US-10-032-189-77	Sequence 77, Appl
21	1306	95.9	267	4 US-10-032-189-77	Sequence 223, App
22	1306	95.9	267	4 US-10-032-189-77	Sequence 230, App
23	1306	95.9	267	5 US-10-032-189-77	Sequence 18, Appl
24	1306	95.9	267	5 US-10-032-189-77	Sequence 23, Appl
25	1306	95.9	267	6 US-11-017-059-16	Sequence 16, Appl
26	1306	95.9	267	6 US-11-017-059-16	Sequence 16, Appl
27	1299	95.4	267	4 US-10-032-189-78	Sequence 78, Appl

28	1286	94.4	276	5 US-10-987-454-199	Sequence 199, App
29	1286	94.4	518	5 US-10-987-454-160	Sequence 160, App
30	1286	94.4	518	5 US-10-987-454-170	Sequence 170, App
31	1285	94.3	524	5 US-10-987-454-203	Sequence 203, App
32	1285	94.3	526	5 US-10-987-454-207	Sequence 207, App
33	1285	94.3	528	5 US-10-987-454-212	Sequence 212, App
34	1285	94.3	530	5 US-10-987-454-216	Sequence 216, App
35	1284	94.3	462	5 US-10-987-454-194	Sequence 194, App
36	1284	94.3	562	5 US-10-987-454-221	Sequence 221, App
37	1284	94.3	566	5 US-10-987-454-229	Sequence 229, App
38	1282	94.1	424	5 US-10-987-454-181	Sequence 181, App
39	1282	94.1	666	5 US-10-987-454-156	Sequence 156, App
40	1281	94.1	249	4 US-10-032-189-76	Sequence 76, Appl
41	1281	94.1	249	4 US-10-032-189-76	Sequence 220, App
42	1281	94.1	249	4 US-10-032-189-76	Sequence 227, App
43	1281	94.1	251	5 US-10-987-454-176	Sequence 176, App
44	1281	94.1	464	5 US-10-987-454-185	Sequence 185, App
45	1281	94.1	493	5 US-10-987-454-151	Sequence 151, App

ALIGNMENTS

RESULT 1
US-09-803-918A-2
; Sequence 2, Application US/09803918A
; Patent No. US20020064820A1
; GENERAL INFORMATION:
; APPLICANT: Dayer, Jean-Michel
; APPLICANT: Burger, Danielle
; APPLICANT: Kohno, Tadahiko
; APPLICANT: Edwards III, Carl K.
; TITLE OF INVENTION: APO-A-1 REGULATION OF T-CELL SIGNALING
; FILE REFERENCE: 06843.0035-00000
; CURRENT APPLICATION NUMBER: US/09/803,918A
; PRIORITY FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/189,008
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/193,551
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-803-918A-2

Query Match	100.0%	Score 1362;	DB 3;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 1e-92;	Mismatches 0;	Indels 0;
Matches 267;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKAAVLTAVLFLTGSQARHFQDEPPQSPDVRVKDLATVYVDVVKDGRDYVSQFEGS	60	
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QY	61	ALGKQLNKLNDWNSVTSTFSKLRQGLPVPTQBFNDNLEKETEGLRQMSKLEEVKAK	120	
DB	61	ALGKQLNKLNDWNSVTSTFSKLRQGLPVPTQBFNDNLEKETEGLRQMSKLEEVKAK	120	
QY	121	VQPYLDFFQKXQEMELRYQKVEPLAELOEGAROKLHELQELKSLPIGEMRDRARAHV	180	
DB	121	VQPYLDFFQKXQEMELRYQKVEPLAELOEGAROKLHELQELKSLPIGEMRDRARAHV	180	
QY	181	DALRTHLAPYSDELRQRLAARLEALKENGGRARLAEYHAKATEHLSTLSEKAKPALEDLRQ	240	
DB	181	DALRTHLAPYSDELRQRLAARLEALKENGGRARLAEYHAKATEHLSTLSEKAKPALEDLRQ	240	
QY	241	GLLPVLESFKVSFLSALREYTKLNTQ	267	
DB	241	GLLPVLESFKVSFLSALREYTKLNTQ	267	

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RESULT 2
US-09-987-107-15
; Sequence 15, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-15

Query Match 100.0%; Score 1362; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

Qy 61 ALGQNLNKLDDNWDVSTSTFSLKREQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGQNLNKLDDNWDVSTSTFSLKREQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEMRDRARAHV 180

Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267
Db 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267

RESULT 4
US-10-032-189-75
; Sequence 75, Application US/10032189
; Publication No. US20030170630A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Grosse, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Gorman, Linda
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Rieger, Daniel K
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-228
; CURRENT APPLICATION NUMBER: US/10/032,189
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11

Qy 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60

Qy 61 ALGQNLNKLDDNWDVSTSTFSLKREQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGQNLNKLDDNWDVSTSTFSLKREQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEMRDRARAHV 180

Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267
Db 241 GLLPVLESFKVSFLSALEEYTKKLNQ 267

RESULT 3
US-09-802-640-30
; Sequence 30, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Kieyn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-30

Query Match 100.0%; Score 1362; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
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; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-189-75

Query Match      100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTIAVLFTGSOARHFHQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGS 60
Db 1 MKAAVLTIAVLFTGSOARHFHQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGS 60

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLEQQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLEQQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMDRARAHV 180

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGGRARLAHYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELQRLAARLEALKENGGRARLAHYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALSEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALSEYTKKLNTQ 267

RESULT 5
US-10-283-599-260
; Sequence 260, Application US/10283599
; Publication No. US20030208059A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-283-599-260

Query Match      100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTIAVLFTGSOARHFHQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGS 60
Db 1 MKAAVLTIAVLFTGSOARHFHQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGS 60

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLEQQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLEQQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMDRARAHV 180

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGGRARLAHYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELQRLAARLEALKENGGRARLAHYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy 241 GLLPVLESFKVSFLSALSEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALSEYTKKLNTQ 267

RESULT 6
US-10-403-902A-30
; Sequence 30, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna
; APPLICANT: Klevn, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/802,640
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-403-902A-30

Query Match      100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTIAVLFTGSOARHFHQDEPPQSPWDRVKDLATVYVDVKDSGRDYVSQFEGS 60
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Db 1 MKAAVLTAVLTGSAQHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKHLQEKLSPLGEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKHLQEKLSPLGEMDRARAHV 180
Qy 181 DALRTHLAPYSDLRQRLAARLEALKENGGRARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDLRQRLAARLEALKENGGRARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKLNTQ 267

RESULT 7

US-10-186-288-10
; Sequence 10, Application US/10186288
; Publication No. US20040001810A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger A.
; TITLE OF INVENTION: Compositions and Methods for Treating
; FILE REFERENCE: P-RD 5299
; CURRENT APPLICATION NUMBER: US/10/186,288
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 09/893,366
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-288-10

Query Match 100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAAVLTAVLTGSAQHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQEGS 60
Db 1 MKAAVLTAVLTGSAQHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKHLQEKLSPLGEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKHLQEKLSPLGEMDRARAHV 180
Qy 181 DALRTHLAPYSDLRQRLAARLEALKENGGRARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDLRQRLAARLEALKENGGRARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKLNTQ 267

RESULT 8

US-10-038-854-219
; Sequence 219, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li

; APPLICANT: Wolenc, Adam R
; APPLICANT: Verniet, Corine
; APPLICANT: Eissen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Vellizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Baha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 219
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-219

Query Match 100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAAVLTAVLTGSAQHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQEGS 60
Db 1 MKAAVLTAVLTGSAQHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPVTQSFWDNLEKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKHLQEKLSPLGEMDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKHLQEKLSPLGEMDRARAHV 180

QY 181 DALRTHLAPYSDELQRLAARLEALKENGAGLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELQRLAARLEALKENGAGLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GLLPVLESFKVSFLSALEBYTKKLTNQ 267
Db 241 GLLPVLESFKVSFLSALEBYTKKLTNQ 267

RESULT 9

US-10-038-854-226
; Sequence 226, Application US/10038854
; Publication No. US20040022781A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eissen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderma, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennnda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854

; CURRENT FILING DATE: 2003-01-22

; PRIOR APPLICATION NUMBER: 60/258,928

; PRIOR FILING DATE: 2000-12-29

; PRIOR APPLICATION NUMBER: 60/259,415

; PRIOR FILING DATE: 2001-01-02

; PRIOR APPLICATION NUMBER: 60/259,785

; PRIOR FILING DATE: 2001-01-04

; PRIOR APPLICATION NUMBER: 60/269,814

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/279,832

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,833

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/279,863

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/283,889

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,447

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/286,683

; PRIOR FILING DATE: 2001-04-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 411

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 226

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Homo sapiens

;

US-10-038-854-226

Query Match 100.0%; Score 1362; DB 4; Length 267;

Best Local Similarity 100.0%; Pred. No. 1e-92;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAVLTIAVLFTGSGARHFQQDEPPQSPWDRVKDLATVVDVLDKSGRDYVSQFEGS 60

Db 1 MKAAVLTIAVLFTGSGARHFQQDEPPQSPWDRVKDLATVVDVLDKSGRDYVSQFEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSFTSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Db 61 ALGKQLNLKLLDNWDSVTSFTSKLRQGLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK 120

QY 121 VQPIYDDFQKQWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPILGEMRDRARAHV 180

Db 121 VQPIYDDFQKQWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPILGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRLAARLEALKENGAGLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELQRLAARLEALKENGAGLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALEBYTKKLTNQ 267

Db 241 GLLPVLESFKVSFLSALEBYTKKLTNQ 267

RESULT 10

US-10-991-217-260

; Sequence 260, Application US/10991217

; Publication No. US20050148513A1

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: GENE THERAPY APPROACHES TO

; TITLE OF INVENTION: SUPPLY APOLOPOPROTEIN A-I AGONISTS AND THEIR

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/991,217

; FILING DATE: 16-NOV-2004

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/940,136

; FILING DATE: 29-SEP-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0007-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 260:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

;

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-991-217-260

Query Match 100.0%; Score 1362; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAAVLTAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPTQSFQFNDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPTQSFQFNDNLEKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLGEMRDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267

RESULT 11

US-10-987-454-2
; Sequence 2, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-454-2

Query Match 100.0%; Score 1362; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAAVLTAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPTQSFQFNDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPTQSFQFNDNLEKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLGEMRDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267

RESULT 12

US-11-017-037-15
; Sequence 15, Application US/11017037
; Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-037-15

Query Match 100.0%; Score 1362; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAAVLTAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Db 1 MKAAVLTAVLFLTGSGARHFQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPTQSFQFNDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFKLREQLGPTQSFQFNDNLEKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQEKLSPLGEMRDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLNTQ 267

RESULT 13

US-11-019-829-15
; Sequence 15, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15

; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: apolipoprotein A-I
; LOCATION: (1)..(267)
; OTHER INFORMATION: M27875.1
US-11-019-829-15

Query Match 100.0%; Score 1362; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Db 1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPGVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPGVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPIDGEEMRDRARHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPIDGEEMRDRARHV 180
Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

RESULT 14
US-11-017-059-15
; Sequence 15, Application US/11017059
; Publication No. US20050142639A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-059-15

Query Match 100.0%; Score 1362; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Db 1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPGVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPGVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120

Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPIDGEEMRDRARHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPIDGEEMRDRARHV 180
Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267
Db 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267

RESULT 15
US-10-852-705A-4
; Sequence 4, Application US/10852705A
; Publication No. US20050191639A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; TITLE OF INVENTION: Method to isolate genes involved in aging
; FILE REFERENCE: RCO/FAC/V098
; CURRENT APPLICATION NUMBER: US/10/852,705A
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: EP01204600.9
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 4
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human APOA1 cDNA fragment
US-10-852-705A-4

Query Match 100.0%; Score 1362; DB 5; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
Db 9 MKAAVLTTLAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQFEGS 68
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPGVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 120
Db 69 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPGVTOEFWDNLEKETEGLRQEMSKDLEEVKAK 128
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPIDGEEMRDRARHV 180
Db 129 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPIDGEEMRDRARHV 188
Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 189 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 248
Qy 241 GLLPVLESFKVSFLSALAEYTKKLNQ 267
Db 249 GLLPVLESFKVSFLSALAEYTKKLNQ 275

Search completed: March 28, 2006, 20:42:42
Job time : 164 secs

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OM protein - protein search, using sw model

Run on: March 28, 2006, 20:27:48 ; Search time 47 Seconds
(without alignments)
469.668 Million cell updates/sec

Title: US-09-803-918A-2

Perfect score: 1362

Sequence: 1 MKAVALTLAVFLTGQARH.....SPKVSFLSALBEYTKLNTQ 267

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep:*
 - 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
 - 3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
 - 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
 - 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	267	1	US-07-959-946-3
2	1362	100.0	267	1	US-08-333-577-3
3	1362	100.0	267	2	US-08-952-796-2
4	1362	100.0	267	2	US-08-940-136-260
5	1362	100.0	267	2	US-10-283-599-260
6	1362	100.0	267	2	US-09-987-107-15
7	1362	100.0	267	4	PCT-US92-08634-3
8	1346	98.8	267	2	US-09-919-039-27
9	1306	95.9	267	2	US-09-987-107-16
10	1246.5	91.5	306	2	US-09-987-107-9
11	1246	91.5	304	2	US-09-987-107-7
12	1246	91.5	304	2	US-09-987-107-8
13	1246	91.5	323	2	US-09-987-107-58
14	1246	91.5	323	2	US-09-987-107-60
15	1243.5	91.3	304	2	US-09-987-107-6
16	1243.5	91.3	306	2	US-09-987-107-10
17	1243.5	91.3	306	2	US-09-987-107-11
18	1243.5	91.3	323	2	US-09-987-107-56
19	1242.5	91.2	337	2	US-09-987-107-46
20	1242	91.2	301	2	US-09-987-107-3
21	1242	91.2	301	2	US-09-987-107-5
22	1242	91.2	316	2	US-09-987-107-48
23	1242	91.2	316	2	US-09-987-107-54
24	1242	91.2	329	2	US-09-987-107-14
25	1242	91.2	344	2	US-09-987-107-68
26	1241	91.1	243	2	US-09-079-030-119
27	1241	91.1	243	2	US-09-987-107-1

Query Match 100.0%; Score 1362; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109;

28	1241	91.1	244	2	US-09-987-107-2	Sequence 2, Appli
29	1241	91.1	261	2	US-09-987-107-52	Sequence 52, Appli
30	1241	91.1	336	2	US-09-987-107-44	Sequence 44, Appli
31	1240.5	91.1	264	1	US-08-448-606-6	Sequence 6, Appli
32	1238	90.9	324	2	US-09-987-107-62	Sequence 62, Appli
33	1235	90.7	324	2	US-09-987-107-64	Sequence 64, Appli
34	1235	90.7	324	2	US-09-987-107-66	Sequence 66, Appli
35	1161.5	85.3	266	2	US-09-987-107-19	Sequence 19, Appli
36	1105	81.1	265	2	US-09-987-107-18	Sequence 18, Appli
37	1100.5	80.8	266	2	US-09-987-107-20	Sequence 20, Appli
38	1077	79.1	265	2	US-09-987-107-17	Sequence 17, Appli
39	1016	74.6	258	2	US-09-987-107-4	Sequence 4, Appli
40	1016	74.6	273	2	US-09-987-107-50	Sequence 50, Appli
41	1006	73.9	200	2	US-08-952-796-15	Sequence 15, Appli
42	975.5	71.6	265	2	US-09-987-107-21	Sequence 21, Appli
43	904.5	66.4	264	2	US-09-987-107-22	Sequence 22, Appli
44	842.5	61.9	259	2	US-09-987-107-23	Sequence 23, Appli
45	727.5	53.4	241	2	US-09-987-107-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-07-959-946-3
; Sequence 3, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wittum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milmanow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-959-946-3

	Matches	267;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MKA	A V L T A V L F T G S Q A R H F W O D E P P Q S D R V K D L A T Y V Y D V L K D S G R D Y V V S Q P E G S	60						
Dd	1	MKA	A V L T A V L F T G S Q A R H F W O D E P P Q S D R V K D L A T Y V Y D V L K D S G R D Y V V S Q P E G S	60						
Qy	61	ALG	K O L N L K L L D N W D S V T I S F S K L R E Q L G P V T Q B F W D N L E K E T E G L R Q E M S K D L E E Y K A K	120						
Dd	61	ALG	K O L N L K L L D N W D S V T I S F S K L R E Q L G P V T Q B F W D N L E K E T E G L R Q E M S K D L E E Y K A K	120						
Qy	121	VQ	P Y L D D F Q K W Q E M E L Y R Q K V E P L R A E L Q E G A R Q K L H E L Q E K L S P L G E M R D R A R A H V	180						
Dd	121	VQ	P Y L D D F Q K W Q E M E L Y R Q K V E P L R A E L Q E G A R Q K L H E L Q E K L S P L G E M R D R A R A H V	180						
Qy	181	D A L R T H L A P Y S D E L Q R L A A R L E A L K E N G G A R L A E Y H A K A T E H L S T I S E K A K P A L E D L R Q	240							
Dd	181	D A L R T H L A P Y S D E L Q R L A A R L E A L K E N G G A R L A E Y H A K A T E H L S T I S E K A K P A L E D L R Q	240							
Qy	241	G L I P V L E S F K V S F L S A L E E Y T K K L N T Q	267							
Dd	241	G L I P V L E S F K V S F L S A L E E Y T K K L N T Q	267							

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RESULT 2
US-08-333-577-3
; Sequence 3, Application US/08333577
; Patent No. 5786206
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
;                           Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,577
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ganson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 234.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-333-577-3

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RESULT 3
US-08-952-796-2
: Sequence 2, Application US/08952796
: Patent No. 6258596
: GENERAL INFORMATION:
: APPLICANT: BENOIT, Patrick
: APPLICANT: BRUCKERT, Eric
: APPLICANT: DENEFFE, Patrice
: APPLICANT: DUBERGER, Nicolas
: APPLICANT: FRUCHART, Jean-Charles
: APPLICANT: LUC, Gerald
: APPLICANT: TURPIN, Gerrard
: APPLICANT: ASSMANN, Gerd
: APPLICANT: FUNKE, Harald
: TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rhone-Poulenc Rorer Inc.
: STREET: 500 Arcola Road, Mailstop 3c43
: CITY: Collegeville
: STATE: PA
: COUNTRY: USA
: ZIP: 19426
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/952,796
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 95/06061
: FILING DATE: 22-MAY-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO FR96/00747
: FILING DATE: 20-MAY-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Fehner Esq., Paul F.
: REGISTRATION NUMBER: 35,135
: REFERENCE/DOCKET NUMBER: ST95031-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610) 454-3839
: TELEFAX: (610) 454-3808
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 267 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-952-796-2

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Query Match 100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60
DB 1 MKAAYLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120
DB 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180
DB 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALREYTKKLNQ 267
DB 241 GLLPVLESFKVSFLSALREYTKKLNQ 267

RESULT 4

US-08-940-136-260
; Sequence 260, Application US/08940136
; Patent No. 6518412

GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-940-136-260

Query Match 100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60
DB 1 MKAAYLTAVLFLTGSQARHFQQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSQPEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120
DB 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

QY 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180
DB 121 VQPYLDDFQKKWQEMELRYQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALREYTKKLNQ 267
DB 241 GLLPVLESFKVSFLSALREYTKKLNQ 267

RESULT 5

US-10-283-599-260
; Sequence 260, Application US/10283599
; Patent No. 6844327

GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-283-599-260

Query Match 100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0;

Qy 1 MKAAVLTIAVLFLTGSGARHFWDQDEPPQSPWDRVKDLATVYVDVKDSGRDYYVSQFEGS 60
Db 1 MKAAVLTIAVLFLTGSGARHFWDQDEPPQSPWDRVKDLATVYVDVKDSGRDYYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWNLKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWNLKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEMRDRARAHV 180
Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALEYTKKLNQ 267
Db 241 GLLPVLESFKVSFLSALEYTKKLNQ 267

RESULT 6

US-09-987-107-15
; Sequence 15, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-15

Query Match 100.0%; Score 1362; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0;

Qy 1 MKAAVLTIAVLFLTGSGARHFWDQDEPPQSPWDRVKDLATVYVDVKDSGRDYYVSQFEGS 60
Db 1 MKAAVLTIAVLFLTGSGARHFWDQDEPPQSPWDRVKDLATVYVDVKDSGRDYYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWNLKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWNLKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEMRDRARAHV 180

Qy 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Qy 241 GLLPVLESFKVSFLSALEYTKKLNQ 267
Db 241 GLLPVLESFKVSFLSALEYTKKLNQ 267

RESULT 7

PCT-US92-08634-3
; Sequence 3, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08634
; FILING DATE: 19921009
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-08634-3

Query Match 100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.6e-109; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0;

Qy 1 MKAAVLTIAVLFLTGSGARHFWDQDEPPQSPWDRVKDLATVYVDVKDSGRDYYVSQFEGS 60
Db 1 MKAAVLTIAVLFLTGSGARHFWDQDEPPQSPWDRVKDLATVYVDVKDSGRDYYVSQFEGS 60
Qy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWNLKETEGLRQEMSKDLEEVKAK 120
Db 61 ALGKQLNLKLLDNWDSVTSTFSKLRQGLPVTQEFWNLKETEGLRQEMSKDLEEVKAK 120
Qy 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEMRDRARAHV 180
Db 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEMRDRARAHV 180

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; CROATISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: misc.feature
; LOCATION: (1)..(58)
;
; OTHER INFORMATION: Trimerisation module from tetranectin
;
; NAME/KEY: misc.feature
; LOCATION: (59)..(63)
;
; OTHER INFORMATION: Linker
;
; NAME/KEY: misc.feature
; LOCATION: (64)..(306)
;
; OTHER INFORMATION: Mature Apo A1
;
US-09-987-107-9

Query Match          91.5%; Score 1246.5; DB 2; Leng
Best Local Similarity 95.0%; Pred. NO. 8e-99;
Matches 247; Conservative 3; Mismatches 7; Indel

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105	LKLLDNWDSVTSTFSKLRQLGPGVPTQBFWDNLSEKTEGLRQENSKOLEEYKAKVQPYLDD	164
Db		
128	FOKKQOEEMELYRQKVPEPIRAELQEGARQKHLHLOEKLSPGLGEMDRARAHVDALRTHL	187
Qy		
165	FOKKQOEEMELYRQKVPEPIRAELQEGARQKHLHLOEKLSPGLGEMDRARAHVDALRTHL	224
Db		
188	APYSDELQRLAARLEALKENGGRARLAEYHAKATEHLSTLSEKAPALDELQGLLPVLE	247
Qy		
225	APYSDELQRLAARLEALKENGGRARLAEYHAKATEHLSTLSEKAPALDELQGLLPVLE	284
Db		
248	SPKVSFLSALBEYTKLNTQ	267
Qy		
285	SPKVSFLSALBEYTKLNTQ	304
Db		

Search completed: March 28, 2006, 20:29:10
Job time : 47 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: March 28, 2006, 20:40:08 ; Search time 24 Seconds
(without alignments)
328.125 Million cell updates/sec

Title: US-09-803-918A-2
Perfect score: 1362
Sequence: 1 MKAALVTLAVLPLTGSQARH.....SFKVSFLSALAEYTKLNTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA New:*
- 1: /SIDSS/prodata/1/pubpaa/US08_NEW_PUB.pap:*
 - 2: /SIDSS/prodata/1/pubpaa/US06_NEW_PUB.pap:*
 - 3: /SIDSS/prodata/1/pubpaa/US07_NEW_PUB.pap:*
 - 4: /SIDSS/prodata/1/pubpaa/US09_NEW_PUB.pap:*
 - 5: /SIDSS/prodata/1/pubpaa/US09_NEW_PUB.pap:*
 - 6: /SIDSS/prodata/1/pubpaa/US10_NEW_PUB.pap:*
 - 7: /SIDSS/prodata/1/pubpaa/US11_NEW_PUB.pap:*
 - 8: /SIDSS/prodata/1/pubpaa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1276	93.7	250	5	US-09-990-087-2
2	1262.5	92.7	301	7	US-11-116-319-2
3	1257.5	92.3	258	7	US-11-116-319-19
4	1257.5	92.3	258	7	US-11-116-319-23
5	1256.5	92.3	258	7	US-11-116-319-21
6	1258.5	92.2	258	7	US-11-116-319-22
7	1254.5	92.1	258	7	US-11-116-319-20
8	1241	91.1	243	7	US-11-006-119-18
9	1241	91.1	243	7	US-11-116-319-1
10	1241	91.1	243	7	US-11-189-438-2
11	1233	90.5	243	7	US-11-189-438-3
12	1233	90.5	243	7	US-11-189-438-4
13	1229	90.2	243	7	US-11-189-438-1
14	1024	75.2	414	5	US-09-990-087-17
15	1019	74.8	422	5	US-09-990-087-19
16	1014.5	74.5	212	5	US-09-990-087-6
17	1010	74.2	201	5	US-09-990-087-9
18	956.5	70.2	392	5	US-09-990-087-45
19	947	69.5	201	5	US-09-990-087-43
20	945	69.4	201	5	US-09-990-087-44
21	761.5	55.9	168	5	US-09-990-087-23
22	759.5	55.8	168	5	US-09-990-087-29
23	733	53.8	160	6	US-10-475-075-171
24	327	24.0	67	7	US-11-055-309A-17
25	318	23.3	65	6	US-10-475-075-457

ALIGNMENTS

RESULT 1
US-09-990-087-2
; Sequence 2, Application US/09990087
; Publication No. US20060057662A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Steven
; APPLICANT: Bayburt, Timothy
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00
; CURRENT APPLICATION NUMBER: US/09/990,087
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-087-2

Query Match	93.7%	Score 1276;	DB 5;	Length 250;
Best Local Similarity	100.0%	Pred. No. 1.2e-79;		
Matches 248;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	20	HFWQDEPPQSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNKLKLLDNWDSVTS	79	
Db	3	HFWQDEPPQSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNKLKLLDNWDSVTS	62	
Qy	80	TFSKLRQLQGPVTOEFWDNLKETEGRLOEMSKDLEEVKAKVQPYLDDFQKKQWQEMELY	139	
Db	63	TFSKLRQLQGPVTOEFWDNLKETEGRLOEMSKDLEEVKAKVQPYLDDFQKKQWQEMELY	122	
Qy	140	RQKVEPLRAELQEGARQKLHELOKLSPLGEMDRARAHVDAURTHLAPYSDLRORLA	199	
Db	123	RQKVEPLRAELQEGARQKLHELOKLSPLGEMDRARAHVDAURTHLAPYSDLRORLA	182	
Qy	200	ARLEALKENGARLAAYHAKATEHLSTLSKAKPALEDLROGLLPVLESFKVSFLSALAE	259	
Db	183	ARLEALKENGARLAAYHAKATEHLSTLSKAKPALEDLROGLLPVLESFKVSFLSALAE	242	
Qy	260	YTKKLNTQ	267	
Db	243	YTKKLNTQ	250	

RESULT 2
US-11-116-319-2

; Sequence 2, Application US/11116319
 ; Publication No. US20050287636A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology
 ; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of
 ; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and
 ; TITLE OF INVENTION: anti-hyperlipidemia
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/11/116.319
 ; CURRENT FILING DATE: 2005-04-28
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Kopatentin 1.71
 ; SEQ ID NO 2
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-116-319-2

Query Match 92.7%; Score 1262.5; DB 7; Length 301;
 Best Local Similarity 97.3%; Pred. No. 1.2e-78;
 Matches 248; Conservative 0; Mismatches 0; Indels 7; Gaps 1;
 Qy 20 HFQQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
 Db 47 HFQQQAPRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 106
 Qy 73 NWDSTVSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLBEVKAKVQPYLDDFOKKW 132
 Db 107 NWDSTVSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLBEVKAKVQPYLDDFOKKW 166
 Qy 133 QEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGSEMRDRARAHVDALRTHLAPYSD 192
 Db 167 QEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGSEMRDRARAHVDALRTHLAPYSD 226
 Qy 193 ELRQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVS 252
 Db 227 ELRQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVS 286
 Qy 253 FLSALEEYTKKLNQ 267
 Db 287 FLSALEEYTKKLNQ 301

RESULT 3
 US-11-116-319-19
 ; Sequence 19, Application US/11116319
 ; Publication No. US20050287636A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology
 ; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of
 ; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and
 ; TITLE OF INVENTION: anti-hyperlipidemia
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/11/116.319
 ; CURRENT FILING DATE: 2005-04-28
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Kopatentin 1.71
 ; SEQ ID NO 19
 ; LENGTH: 258
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: proapoA-I-A154E
 US-11-116-319-19

Query Match 92.3%; Score 1257.5; DB 7; Length 258;
 Best Local Similarity 96.9%; Pred. No. 2.2e-78;
 Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
 Qy 20 HFQQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
 Db 4 HFQQQAPRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63

Qy 73 NWDSTVSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLBEVKAKVQPYLDDFOKKW 132
 Db 64 NWDSTVSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLBEVKAKVQPYLDDFOKKW 123
 Qy 133 QEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGSEMRDRARAHVDALRTHLAPYSD 192
 Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGSEMRDRARAHVDALRTHLAPYSD 183
 Qy 193 ELRQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVS 252
 Db 184 ELRQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVS 243
 Qy 253 FLSALEEYTKKLNQ 267
 Db 244 FLSALEEYTKKLNQ 258

RESULT 4
 US-11-116-319-23
 ; Sequence 23, Application US/11116319
 ; Publication No. US20050287636A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology
 ; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of
 ; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and
 ; TITLE OF INVENTION: anti-hyperlipidemia
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/11/116.319
 ; CURRENT FILING DATE: 2005-04-28
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Kopatentin 1.71
 ; SEQ ID NO 23
 ; LENGTH: 258
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: proapoA-I-A158E
 US-11-116-319-23

Query Match 92.3%; Score 1257.5; DB 7; Length 258;
 Best Local Similarity 96.9%; Pred. No. 2.2e-78;
 Matches 247; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
 Qy 20 HFQQQ-----DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 72
 Db 4 HFQQQAPRPPTPDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLD 63
 Qy 73 NWDSTVSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLBEVKAKVQPYLDDFOKKW 132
 Db 64 NWDSTVSTFSKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLBEVKAKVQPYLDDFOKKW 123
 Qy 133 QEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGSEMRDRARAHVDALRTHLAPYSD 192
 Db 124 QEEMELYRQKVEPLRAELQEGARQKLHELOEKLSPGSEMRDRARAHVDALRTHLAPYSD 183
 Qy 193 ELRQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVS 252
 Db 184 ELRQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLRQGLLPVLESFKVS 243
 Qy 253 FLSALEEYTKKLNQ 267
 Db 244 FLSALEEYTKKLNQ 258

RESULT 5
 US-11-116-319-21
 ; Sequence 21, Application US/11116319
 ; Publication No. US20050287636A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korea Research Institutes of Bioscience and Biotechnology
 ; TITLE OF INVENTION: Prophylactic and therapeutic agents containing point mutants of
 ; TITLE OF INVENTION: proapolipoprotein A-I for anti-atherosclerosis and
 ; TITLE OF INVENTION: anti-hyperlipidemia

; PRIOR APPLICATION NUMBER: US 60/590,689
; PRIOR FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-189-438-3

Query Match 90.5%; Score 1233; DB 7; Length 243;
Best Local Similarity 99.6%; Pred. No. 9.4e-77;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 DEPPQSPWDRVKDLATVYVVLKDSGRDYVSQFGSALGKQLNLKLLDNWDSVTSTFSKL 84
DB 1 DEPPQSPWDRVKDLATVYVVLKDSGRDYVSQFGSALGKQLNLKLLDNWDSVTSTFSKL 60
QY 85 REQLGPVTQEFWDNLEKETEGRLQEMSKDLBEVKAKVQPYLDDFKKKQWQEMELYRQKVE 144
DB 61 REQLGPVTQEFWDNLEKETEGRLQEMSKDLBEVKAKVQPYLDDFKKKQWQEMELYRQKVE 120
QY 145 PLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 204
DB 121 PLRAELQEGARQKLHELQEKLSPLGEMRDCARAHVDALRTHLAPYSDELRLQRLAARLEA 180
QY 205 LKENGARLAAYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKVSFLSALBEYTKKL 264
DB 181 LKENGARLAAYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKVSFLSALBEYTKKL 240
QY 265 NTQ 267
DB 241 NTQ 243

RESULT 12

US-11-189-438-4

; Sequence 4, Application US/11189438
; Publication No. US20060030525A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Moore, Gregory
; TITLE OF INVENTION: APOLIPOPROTEIN A-I DERIVATIVES WITH ALTERED IMMUNOGENICITY
; FILE REFERENCE: 186832/US/2
; CURRENT APPLICATION NUMBER: US/11/189,438
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: US 60/590,689
; PRIOR FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 4
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-189-438-4

Query Match 90.5%; Score 1233; DB 7; Length 243;
Best Local Similarity 99.6%; Pred. No. 9.4e-77;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 DEPPQSPWDRVKDLATVYVVLKDSGRDYVSQFGSALGKQLNLKLLDNWDSVTSTFSKL 84
DB 1 DEPPQSPWDRVKDLATVYVVLKDSGRDYVSQFGSALGKQLNLKLLDNWDSVTSTFSKL 60
QY 85 REQLGPVTQEFWDNLEKETEGRLQEMSKDLBEVKAKVQPYLDDFKKKQWQEMELYRQKVE 144
DB 61 REQLGPVTQEFWDNLEKETEGRLQEMSKDLBEVKAKVQPYLDDFKKKQWQEMELYRQKVE 120
QY 145 PLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 204
DB 121 PLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 180
QY 205 LKENGARLAAYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKVSFLSALBEYTKKL 264

DB 181 LKENGARLAAYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKVSFLSALBEYTKKL 240
QY 265 NTQ 267
DB 241 NTQ 243

RESULT 13

US-11-189-438-1

; Sequence 1, Application US/11189438
; Publication No. US20060030525A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Moore, Gregory
; TITLE OF INVENTION: APOLIPOPROTEIN A-I DERIVATIVES WITH ALTERED IMMUNOGENICITY
; FILE REFERENCE: 186832/US/2
; CURRENT APPLICATION NUMBER: US/11/189,438
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: US 60/590,689
; PRIOR FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (151)..(151)
; OTHER INFORMATION: Xaa can be Arginine or Cysteine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: Xaa can be Arginine or Cysteine
US-11-189-438-1

Query Match 90.2%; Score 1229; DB 7; Length 243;
Best Local Similarity 99.2%; Pred. No. 1.8e-76;
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 DEPPQSPWDRVKDLATVYVVLKDSGRDYVSQFGSALGKQLNLKLLDNWDSVTSTFSKL 84
DB 1 DEPPQSPWDRVKDLATVYVVLKDSGRDYVSQFGSALGKQLNLKLLDNWDSVTSTFSKL 60
QY 85 REQLGPVTQEFWDNLEKETEGRLQEMSKDLBEVKAKVQPYLDDFKKKQWQEMELYRQKVE 144
DB 61 REQLGPVTQEFWDNLEKETEGRLQEMSKDLBEVKAKVQPYLDDFKKKQWQEMELYRQKVE 120
QY 145 PLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 204
DB 121 PLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEA 180
QY 205 LKENGARLAAYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKVSFLSALBEYTKKL 264
DB 181 LKENGARLAAYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKVSFLSALBEYTKKL 240
QY 265 NTQ 267
DB 241 NTQ 243

RESULT 14

US-09-950-087-17

; Sequence 17, Application US/09990087
; Publication No. US20060057662A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Steven
; APPLICANT: Bayburt, Timothy
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00

```

; CURRENT APPLICATION NUMBER: US/09/990,087
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; -OTHER INFORMATION: peptide
US-09-990-087-17

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	Query Match	75.2%	Score 1024;	DB 5;	Length 414;
	Best Local Similarity	88.5%;	Pred. No. 2.5e-62;		
	Matches 208;	Conservative	6;	Mismatches 19;	Indels 2; Gaps 1;
QY	35 VKDLATVYVDVKDSDGRDYYQSF--GSA LGKQLNLKLLDNWDSVTSTFSKLRQELGPVT	92			
Db	180 LEDLRQGLLPVLESFKVSFLSALEYTKLNTQGTLLKLLDNWDSVTSTFSKLRQELGPVT	239			
QY	93 QEPWDNLEKETEGLRQEMSKDLBEVKAQVPYLLDDFOKKWQOEMELYRQKVEPLRAELQE	152			
Db	240 QEPWDNLEKETEGLRQEMSKDLBEVKAQVPYLLDDFOKKWQOEMELYRQKVEPLRAELQE	299			
QY	153 GARQKHLHQELKSLPGCEEMDRARAHVDALRTHLAPYSDLRQRLAARLEALKENGAR	212			
Db	300 GARQKHLHQELKSLPGCEEMDRARAHVDALRTHLAPYSDLRQRLAARLEALKENGAR	359			
QY	213 LAEYHAKATHEHLSTLSEKAPPALEDLRQGLLPVLESFKVSFLSALEYTKKLNQ	267			
Db	360 LAEYHAKATHEHLSTLSEKAPPALEDLRQGLLPVLESFKVSFLSALEYTKKLNQ	414			

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RESULT 15
US-09-990-087-19
; Sequence 19, Application US/09990087
; Publication No. US20060057662A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Steven
; APPLICANT: Bayburt, Timothy
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00
; CURRENT APPLICATION NUMBER: US/09/990,087
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-990-087-19

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	Query Match	74.8%	Score 1019;	DB 5;	Length 422;
	Best Local Similarity	85.3%	Pred. No. 5.6e-62;		
	Matches 209;	Conservative	7;	Mismatches 15;	Indels 14; Gaps 2;
Qy	35	VKDLATVYDVVLKDSGRDYVSQFEGSALGQNLN-----LKLDNWDSVTSTFS	82		
		: : : : : : : : : : : : : : :			
Db	180	LEBLRQGLLPLVLSFKVSFLSALE--EYTKLANTQGTGGSGGGTLLKLDNWDSTSTFS	237		
Qy	83	KLREQIGPVVQTEFWDNLKEKTEGLRQMSKDLERVKAKVQPYLLDDFKKKQCEEMELRYQK	142		
Db	238	KLREQIGPVVQTEFWDNLKEKTEGLRQMSKDLERVKAKVQPYLLDDFKKKQCEEMELRYQK	297		
Ov	143	VEPLRAELQEGAKOKLHELQEKLSPLCEEMRDRARAHVDALRTHLAPYSDELRLAARL	202		

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 20:20:38 ; Search time 231 Seconds
(without alignments)
815.481 Million cell updates/sec

Title: US-09-803-918A-2

Perfect score: 1362

Sequence: 1 MKAAVLTLAVLFLTGSQLRH.....SPKVSFLSLEETKILNTQ 267

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	267	1 APOAL_HUMAN	P02647 homo sapien
2	1362	100.0	267	2 Q6Q785_HUMAN	Q6Q785 homo sapien
3	1306	95.9	267	1 APOAL_MACFA	P68292 macaca fasc
4	1306	95.9	267	1 APOAL_PAPHA	P68293 papio hanad
5	1161.5	85.3	266	1 APOAL_CANFA	P02648 canis famil
6	1105	81.1	265	1 APOAL_PIG	P18648 sus scrofa
7	1100.5	80.8	266	1 APOAL_RABIT	P09809 oryctolagus
8	1077	79.1	265	1 APOAL_BOVIN	P15497 bos taurus
9	1012.5	74.3	264	1 APOAL_MESAU	Q92214 mesocricetu
10	975.5	71.6	265	1 APOAL_TURGB	O18759 tupaiia gliis
11	962	70.6	191	2 Q8HZ96_9PRIM	Q8HZ96 gorilla gor
12	962	70.6	191	2 Q8HZ97_PANTR	Q8HZ97 pan troglod
13	947	69.5	191	2 Q8HZ95_PONPY	Q8HZ95 pongo pygma
14	905.5	66.5	264	2 Q8BPDS_MOUSE	Q8BPDS mus musculu
15	904.5	66.4	264	1 APOAL_MOUSE	Q00623 mus musculu
16	896	65.8	263	2 Q08855_MOUSE	Q08855 mus musculu
17	895	65.7	263	2 Q09042_MOUSE	Q09042 mus musculu
18	849.5	62.4	259	2 Q5EBB2_RAT	Q5EBB2 rattus norv
19	842.5	61.9	259	1 APOAL_RAT	P04639 rattus norv
20	836	61.4	258	2 Q09054_RAT	Q09054 rattus norv
21	834	61.2	258	2 Q08877_RAT	Q08877 rattus norv
22	823	60.4	191	2 Q8HZ94_SAGOE	Q8HZ94 saguinus oe
23	727.5	53.4	241	2 Q9TS49_ERIEU	Q9TS49 erinaceus e
24	705.5	51.8	264	1 APOAL_ANAPL	O42296 anas platyr
25	688.5	50.6	264	1 APOAL_CHICK	P08250 gallus gall
26	663.5	48.7	264	1 APOAL_COTUA	P32918 coturnix co
27	616	45.2	198	2 Q58EV2_MOUSE	Q58EV2 mus musculu
28	526	38.6	260	2 Q7ZY85_XENLA	Q7ZY85 xenopus lae
29	519	38.1	260	2 Q7SZA1_XENLA	Q7SZA1 xenopus lae
30	512	37.6	261	2 Q6DDC5_XENTR	Q6DDC5 xenopus tro
31	327	24.0	67	2 Q9Y355_HUMAN	Q9Y355 homo sapien

RESULT 1

ID	AP0AL_HUMAN	STANDARD;	PRT;	267 AA.
AC	P02647; Q6LDN9;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipoprotein A-I(1-242)]			
GN	Name=APOA1;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=83220822; PubMed=6406984;			
RA	Shoulders C.C., Kornblitt A.R., Munro B.S., Baralle F.E.;			
RT	"Gene structure of human apolipoprotein AI.;"			
RL	Nucleic Acids Res. 11:2827-2837(1983).			
[2]				
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=83220772; PubMed=6304641;			
RA	Cheung P., Chan L.;			
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.;"			
RL	Nucleic Acids Res. 11:3703-3715(1983).			
[3]				
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=84015011; PubMed=6413973;			
RA	Karathanasis S.K., Zannis V.I., Breslow J.L.;			
RT	"Isolation and characterization of the human apolipoprotein A-I gene.;"			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).			
[4]				
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=85026665; PubMed=6207999;			
RA	Seilhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.;			
RT	"Isolation and DNA sequence of full-length cDNA and of the entire gene for human apolipoprotein AI -- discovery of a new genetic polymorphism in the apo AI gene.;"			
RL	DNA 3:309-317(1984).			
[5]				
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=84221405; PubMed=6328445;			
RA	Sharpe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C., Baralle F.E.;			
RT	"Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundance.;"			
RL	Nucleic Acids Res. 12:3917-3932(1984).			
[6]				
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=84119464; PubMed=6198645;			
RA	Law S.W., Brewer H.B. Jr.;			

Q6LD50 mus sp. apo
Q29248 sus scrofa
Q6P7H6 xenopus lae
Q5XHD2 xenopus lae
Q6PBB8 xenopus lae
Q640E4 xenopus lae
Q98TG6 anguilla ja
Q66IL6 xenopus tro
P33621 macaca fasc
Q6DHE2 brachydanio
Q567B9 brachydanio
O42363 brachydanio
P06727 homo sapien
Q6Q787 homo sapien

ALIGNMENTS

RT "Nucleotide sequence and the encoded amino acids of human
 RT apolipoprotein A-I mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).
 RN [7].
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86608382; PubMed=2995392;
 RA Law S.W., Brewer H.B. Jr.;
 RT "Tangier disease. The complete mRNA sequence encoding for preproapo-A-
 RL J.";
 RN J. Biol. Chem. 260:12810-12814(1985).
 RP [8].
 RP NUCLEOTIDE SEQUENCE (VARIANT TANGIER).
 RX MEDLINE=88196137; PubMed=3129297;
 RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
 RA Zannis V.I.;
 RT "Sequence and expression of Tangier apoA-I gene.";
 RL Eur. J. Biochem. 173:465-471(1988).
 RN [9].
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89377481; PubMed=2673706;
 RA Moguilevsky N., Roehol C., Loriau R., Guillaume J.P., Jacobs P.,
 RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
 RA Holmquist L., Carlson L.A., Bollen A.;
 RT "Production of human recombinant proapolipoprotein A-I in Escherichia
 RL coli: purification and biochemical characterization.";
 RN DNA 8:429-436(1989).
 RP [10].
 RP NUCLEOTIDE SEQUENCE.
 RA Bollen A., Gobert J., Wuelfert E.;
 RT "Expression of human proapolipoprotein A-1.";
 RL Patent number EP0293357, 30-NOV-1988.
 RN [11].
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12].
 RP PROTEIN SEQUENCE OF 19-27.
 RX MEDLINE=83256553; PubMed=6409108;
 RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Ronan R., Law S.,
 RA Light J.A.;
 RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
 RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
 RN [13].
 RP PROTEIN SEQUENCE OF 25-267.
 RX MEDLINE=75133493; PubMed=164450;
 RA Baker H.N., Gatto A.M. Jr., Jackson R.L.;
 RT "The primary structure of human plasma high density apolipoprotein
 RT glutamine I (ApoA-I). II. The amino acid sequence and alignment of
 RT cyanogen bromide fragments IV, VII, and I.";
 RL J. Biol. Chem. 250:2725-2738(1975).
 RN [14].
 RP PROTEIN SEQUENCE OF 25-267.
 RX MEDLINE=78123731; PubMed=204308;
 RA Brewer H.B. Jr., Fairwell T., Larue A., Ronan R., Houser A.,
 RA Bronzert T.J.;
 RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated
 RT from high density lipoproteins.";
 RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
 RN [15].
 RP PROTEIN SEQUENCE OF 25-56.
 RX MEDLINE=88331387; PubMed=3047170;
 RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
 RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein
 RT A-I (Apo A-I). A novel function of Apo A-I.";
 RL J. Clin. Invest. 82:803-807(1988).
 RN [16].
 RP PROTEIN SEQUENCE OF 25-48.
 RX MEDLINE=89380318; PubMed=2506184;
 RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
 RA Chapdelaine A.;
 RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
 RT proteins.";
 RL J. Biol. Chem. 264:16853-16857(1989).
 RN [17].
 RP PROTEIN SEQUENCE OF 25-43.
 RX MEDLINE=88070603; PubMed=3120314;
 RA Prioli R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
 RA Pereira M.E.A.;
 RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
 RT neuraminidase, to high-density lipoprotein.";
 RL Science 238:1417-1419(1987).
 RN [18].
 RP PROTEIN SEQUENCE OF 25-42.
 RX TISSUE=Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [19].
 RP PROTEIN SEQUENCE OF 25-34.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RN Nat. Biotechnol. 21:566-569(2003).
 RP [20].
 RP NUCLEOTIDE SEQUENCE OF 118-267.
 RX MEDLINE=83091059; PubMed=6294659;
 RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
 RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
 RT "Isolation and characterization of cDNA clones for human
 RT apolipoprotein A-I.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
 RN [21].
 RP PALMITOYLATION.
 RX MEDLINE=86140194; PubMed=3005308;
 RA Hoeg J.M., Meng M.S., Ronan R., Fairwell T., Brewer H.B. Jr.;
 RT "Human apolipoprotein A-I. Post-translational modification by fatty
 RT acid acylation.";
 RL J. Biol. Chem. 261:3911-3914(1986).
 RN [22].
 RP PROCESSING.
 RX MEDLINE=83195100; PubMed=6405383;
 RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
 RA Breslow J.L.;
 RT "Intracellular and extracellular processing of human apolipoprotein A-
 RT I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
 RN [23].
 RP MASS SPECTROMETRY.
 RX MEDLINE=22503077; PubMed=12562854; DOI=10.1194/jlr.D200034-JLR200;
 RA Niderkofler E.B., Tubbs K.A., Kiernan U.A., Nedelkov D., Nelson R.W.;
 RT "Novel mass spectrometric immunoassays for the rapid structural

```
RT  characterization of plasma apolipoproteins." ;
RL  J. Lipid Res. 44:630-639(2003).

Query Match      100.0% ; Score 1362 ; DB 1 ; Length 267 ;
Best Local Similarity 100.0% ; Pred. No. 1.le-64 ;
Matches 267 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Qy  1  MKAAVLTAVLFLTGSOARHFQQDEPPQSPWDRVKDLATVVDVLKDSGRDYVSQFEGS 60
Db  1  MKAAVLTAVLFLTGSOARHFQQDEPPQSPWDRVKDLATVVDVLKDSGRDYVSQFEGS 60

Qy  61  ALGKQLNLKLLDNWDSVTSTSKLREQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120
Db  61  ALGKQLNLKLLDNWDSVTSTSKLREQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

Qy  121  VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180
Db  121  VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180

Qy  181  DALRTHLAPYSDELQRLAARLEALKENGGAARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
Db  181  DALRTHLAPYSDELQRLAARLEALKENGGAARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

Qy  241  GLLPVLESFKVSFLSALSEYTKKLNTQ 267
Db  241  GLLPVLESFKVSFLSALSEYTKKLNTQ 267

RESULT 2
Q6Q785 HUMAN PRELIMINARY ; PRT ; 267 AA.
AC  Q6Q785 ;
DT  10-MAY-2005 (TrEMBLrel. 30, Created)
DT  10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE  Apolipoprotein A-I.
GN  Name=APOA1 ;
OS  Homo sapiens (Human) ;
OC  Eukaryota ; Metazoa ; Chordata ; Craniata ; Vertebrata ; Euteleostomi ;
OC  Mammalia ; Eutheria ; Euarchontoglires ; Primates ; Catarrhini ; Hominidae ;
OC  Homo.
OX  NCBI_TaxID=9606 ;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  PubMed=15108119 ; DOI=10.1007/800439-004-1106-x ;
RA  Fullerton S.M., Buchanan A.V., Sonpar V.A., Taylor S.L., Smith J.D.,
RA  Carlson C.S., Salomaa V., Stengard J.H., Boerwinkle E., Clark A.G.,
RA  Nickerson D.A., Weiss K.M. ;
RT  "The effects of scale: variation in the APOA1/C3/A4/A5 gene cluster." ;
RL  Hum. Genet. 115:36-56(2004).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RA  Nickerson D.A., Smith J.D., Fullerton S.M., Clark A.G., Stengard J.H.,
RA  Salomaa V., Boerwinkle E., Sing C.F., Weiss K.M. ;
RL  Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL ; AY555191 ; AAS68227.1 ; - ; Genomic DNA.
DR  EMBL ; AY422952 ; AAQ91811.1 ; - ; Genomic DNA.
KW  Lipoprotein.
SQ  SEQUENCE 267 AA ; 30778 MW ; 1A28B8365E620310 CRC64 ;

Query Match      100.0% ; Score 1362 ; DB 2 ; Length 267 ;
Best Local Similarity 100.0% ; Pred. No. 1.le-64 ;
Matches 267 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Qy  1  MKAAVLTAVLFLTGSOARHFQQDEPPQSPWDRVKDLATVVDVLKDSGRDYVSQFEGS 60
Db  1  MKAAVLTAVLFLTGSOARHFQQDEPPQSPWDRVKDLATVVDVLKDSGRDYVSQFEGS 60

Qy  61  ALGKQLNLKLLDNWDSVTSTSKLREQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120
Db  61  ALGKQLNLKLLDNWDSVTSTSKLREQLGPGVPTQEFWDLNLEKETEGRLQEMSKDLEEVKAK 120

Qy  121  VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180
Db  121  VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGHEMRDRARAHV 180

RESULT 3
APOA1 MACFA STANDARD ; PRT ; 267 AA.
AC  P68292 ; P15568 ; P17929 ;
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) .
GN  Name=APOA1 ;
OS  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey) .
OC  Eukaryota ; Metazoa ; Chordata ; Craniata ; Vertebrata ; Euteleostomi ;
OC  Mammalia ; Eutheria ; Euarchontoglires ; Primates ; Catarrhini ;
OC  Cercopitheidae ; Cercopitheinae ; Macaca.
OX  NCBI_TaxID=9541 ;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=87191989 ; PubMed=3106152 ; DOI=10.1016/0378-1119(86)90389-6 ;
RA  Polites H.G., Melchior G.W., Castle C.K., Marotti K.R. ;
RT  "The primary structure of cynomolgus monkey apolipoprotein A-1 deduced
RT  from the cDNA sequence: comparison to the human sequence." ;
RL  Gene 49:103-110(1986).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=92305062 ; PubMed=1610902 ; DOI=10.1016/0167-4781(92)90079-F ;
RA  Murray R.W., Marotti K.R. ;
RT  "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
RT  and corresponding flanking regions." ;
RL  Biochim. Biophys. Acta 1131:207-210(1992).
RN  [3]
RP  NUCLEOTIDE SEQUENCE OF 1-10.
RX  PubMed=1917942 ;
RA  Sorci-Thomas M., Kearns M.W. ;
RT  "Transcriptional regulation of the apolipoprotein A-I gene. Species-
RT  specific expression correlates with rates of gene transcription." ;
RL  J. Biol. Chem. 266:18045-18050(1991).
RN  [4]
RP  PROTEIN SEQUENCE OF 25-48.
RX  MEDLINE=87185451 ; PubMed=3105581 ;
RA  Herbert P.N., Bausserman L.L., Lynch K.M., Saritelli A.L.,
RA  Kantor M.A., Nicolosi R.J., Shulman R.S. ;
RT  "Homologues of the human C and A apolipoproteins in the Macaca
RT  fascicularis (cynomolgus) monkey." ;
RL  Biochemistry 26:1457-1463(1987).
CC  -!- FUNCTION: Participates in the reverse transport of cholesterol
CC  efflux from tissues to the liver for excretion by promoting cholesterol
CC  efflux from tissues and by acting as a cofactor for the lecithin
CC  cholesterol acyltransferase (LCAT) .
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC  chylomicrons.
CC  -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  EMBL ; M15411 ; AAA36834.1 ; - ; mRNA.
CC  EMBL ; M83242 ; AAA36832.1 ; - ; Genomic DNA.
CC  EMBL ; M69223 ; AAA36831.1 ; - ; Genomic DNA.
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DR PIR; A26529; A26529.
DR HSSP; P02647; 1GW4.
DR SMR; P68292; 68-267.
DR InterPro; IPR000074; ApoA1 A4 E.
DR PANTHER; PTHR18976; ApoA1 A4 E; 1.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Cholesterol metabolism; Direct protein sequencing; HDL;
KW Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;
KW Steroid metabolism; Transport.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 267 Apolipoprotein A-I.
FT REPEAT 68 89 1.
FT REPEAT 90 111 2.
FT REPEAT 112 122 3 (half-length).
FT REPEAT 123 144 4.
FT REPEAT 145 166 5.
FT REPEAT 167 188 6.
FT REPEAT 189 210 7.
FT REPEAT 211 232 8.
FT REPEAT 233 243 9 (half-length).
FT REPEAT 244 267 10.
FT REGION 68 267 10 X approximate tandem repeats.
FT CONFLICT 13 13 L -> P (in Ref. 1).
SQ SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;

Query Match 95.9%; Score 1306; DB 1; Length 267;
Best Local Similarity 95.1%; Pred. No. 9.9e-62;
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKAAVLTAVLFLTGSOARHFQWQDEPPQSPWDRVKDLATVYVDLKDGRDYVSQEGS 60
DB 1 MKAIVLTLAVLFLTGSOARHFQWQDEPPQTPWDRVKDLVTVYVEALKDSKDYVSQEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQFWDNLEKTEGLRQEMSKOLEEVKAK 120
DB 61 ALGKQLNLKLLDNWDSVTSTVSKLRQLGPVTQFWDNLEKTEGLRQEMSKOLEEVKAK 120

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180
DB 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELQRQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALEYTKKLNTQ 267
DB 241 GLLPVLESFKVSFLSALEYTKKLSTQ 267

RESULT 4
ID APOA1 PAPA STANDARD; PRT; 267 AA.
AC P68293; P15568; P17929;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).
GN Name=APOA1;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=89232739; PubMed=2907746; DOI=10.1016/0378-1119(88)90181-3;
RA Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandeberg J.L.;
RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
RT clone and identification of DNA polymorphisms for genetic studies of
RT cholesterol metabolism.";
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RL Gene 74:483-490 (1988).
CC -I- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
CC cholesterol acyltransferase (LCAT).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons.
CC -I- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M35634; AAA35380.1; -; mRNA.
CC HSSP; P02647; 1GW4.
CC SMR; P68293; 68-267.
CC InterPro; IPR000074; ApoA1 A4 E.
CC PANTHER; PTHR18976; ApoA1 A4 E; 1.
CC Pfam; PF01442; Apolipoprotein; 1.
KW Cholesterol metabolism; HDL; Lipid metabolism; Lipid transport;
KW Plasma; Repeat; Signal; Steroid metabolism; Transport.
FT SIGNAL 1 18
FT PROPEP 19 24 Apolipoprotein A-I.
FT CHAIN 25 267 1.
FT REPEAT 68 89 1.
FT REPEAT 90 111 2.
FT REPEAT 112 122 3 (half-length).
FT REPEAT 123 144 4.
FT REPEAT 145 166 5.
FT REPEAT 167 188 6.
FT REPEAT 189 210 7.
FT REPEAT 211 232 8.
FT REPEAT 233 243 9 (half-length).
FT REPEAT 244 267 10.
FT REGION 68 267 10 X approximate tandem repeats.
SQ SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;

Query Match 95.9%; Score 1306; DB 1; Length 267;
Best Local Similarity 95.1%; Pred. No. 9.9e-62;
Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKAAVLTAVLFLTGSOARHFQWQDEPPQSPWDRVKDLATVYVDLKDGRDYVSQEGS 60
DB 1 MKAIVLTLAVLFLTGSOARHFQWQDEPPQTPWDRVKDLVTVYVEALKDSKDYVSQEGS 60

QY 61 ALGKQLNLKLLDNWDSVTSTFSKLRQLGPVTQFWDNLEKTEGLRQEMSKOLEEVKAK 120
DB 61 ALGKQLNLKLLDNWDSVTSTVSKLRQLGPVTQFWDNLEKTEGLRQEMSKOLEEVKAK 120

QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180
DB 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDELQRQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELQRQRLAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQ 240

QY 241 GLLPVLESFKVSFLSALEYTKKLNTQ 267
DB 241 GLLPVLESFKVSFLSALEYTKKLSTQ 267

RESULT 5
ID APOA1 CANFA STANDARD; PRT; 266 AA.
AC P02648;
DT 21-JUN-1986 (Rel. 01, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).
```


GN Name=APOA1;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Liver;
 RX MEDLINE=90132271; PubMed=2515239;
 RA Luo C.-C., Li W.-H., Chan L.;
 RT "Structure and expression of dog apolipoprotein A-I, B, and C-I mRNAs:
 RT implications for the evolution and functional constraints of
 RT apolipoprotein structures.";
 RL J. Lipid Res. 30:1735-1746(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 25-266.
 RX MEDLINE=82142425; PubMed=6801039;
 RA Chung H., Randolph A., Reardon I., Heinrikson R.L.;
 RT "The covalent structure of apolipoprotein A-I from canine high density
 RT lipoproteins.";
 RL J. Biol. Chem. 257:2961-2967(1982).
 RN [3]
 RP PROTEIN SEQUENCE OF 25-57 AND 262-265.
 RX MEDLINE=76210910; PubMed=179887; DOI=10.1016/0014-5793(76)80338-9;
 RA Nakai T., Whayne T.F., Fang J.;
 RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein
 RT A-I.";
 RL FEBS Lett. 64:409-411(1976).
 RN [4]
 RP PROTEIN SEQUENCE OF 25-37.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: Participates in the reverse transport of cholesterol
 CC from tissues to the liver for excretion by promoting cholesterol
 CC efflux from tissues and by acting as a cofactor for the lecithin
 CC cholesterol acyltransferase (LCAT).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
 CC chylomicrons. Synthesized in the liver and small intestine.
 CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC PIR: A60940; LPDGM1.
 CC DR HSP; P02647; LAV1.
 CC DR HSC-2DPAGE; P02648; DOG.
 CC DR Ensembl; ENSCAFG00000013320; Canis familiaris.
 CC DR InterPro; IPR000074; APOA1_A4_E.
 CC DR PANTHER; PTHR18976; APOA1_A4_E; 1.
 CC DR Pfam; PF01442; Apolipoprotein; 1.
 CC DR Cholesterol metabolism; Direct protein sequencing; HDL;
 CC Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;
 CC Steroid metabolism; Transport.
 CC
 CC SIGNAL 1 18 By similarity.
 CC FT PROPEP 19 24
 CC FT CHAIN 25 266 Apolipoprotein A-I.
 CC FT REPEAT 67 88 1.
 CC FT REPEAT 89 110 2.
 CC FT REPEAT 111 121 3 (half-length).
 CC FT REPEAT 122 143 4.
 CC FT REPEAT 144 165 5.
 CC FT REPEAT 166 187 6.
 CC FT REPEAT 188 209 7.

FT REPEAT 210 231 8.
 FT REPEAT 232 242 9 (half-length).
 FT REPEAT 243 266 10.
 FT REGION 67 266 10 X approximate tandem repeats.
 FT CONFLICT 168 168 A -> G (in Ref. 2).
 FT CONFLICT 202 202 E -> Q (in Ref. 2).
 FT CONFLICT 235 235 E -> Q (in Ref. 2).
 FT CONFLICT 264 266 NAQ -> A (in Ref. 3).
 SQ SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;
 Query Match 85.3%; Score 1161.5; DB 1; Length 266;
 Best Local Similarity 85.0%; Pred. No. 4.4e-54;
 Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;
 QY 1 MKAAVILAVLFLTGSQARHFQQDEPQSPWDRVKDLATVYDVVLKSGRDYVSQPEGS 60
 DB 1 MKAALLTAVLFLTGSQARHFQQDEPQSPWDRVKDLATVYDVVLKSGRDYVAQFEAS 59
 QY 61 ALGKQLMLKLLDNWDSVTFSKLEQLEQPGVPTQFNDNLEKETEGLRQEMSKDLEEVKAK 120
 DB 60 ALGKQLMLKLLDNWDSLSSTVTKLEQIGPVPTQFNDNLEKETEVLRQEMSKDLEEVKQK 119
 QY 121 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEGEEMRRARAHV 180
 DB 120 VQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEGEEMRRARAHV 179
 QY 181 DALRTHLAPYSDLELRLARLEALKENGGRARLARYHAKATEHLSTLSEKAKPALEDLRQ 240
 DB 180 DALRAQLAPYSDLLRLRLARLEALKENGGRARLARYHAKATEHLSTLSEKAKPALEDLRQ 239
 QY 241 GLLPVLESFKVSLSALEEVTKLNTQ 267
 DB 240 GLLPVLESFKVSLSALEEVTKLNTQ 266
 RESULT 6
 APOA1_PIG STANDARD; PRT; 265 AA.
 AC P18648;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).
 GN Name=APOA1; (Pig).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93224154; PubMed=8468059;
 RA Birchbauer A., Knipping G., Juritsch B., Aschauer H., Zechner R.;
 RT "Characterization of the apolipoprotein AI and CIII genes in the
 RT domestic pig.";
 RL Genomics 15:643-652(1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=94125128; PubMed=8294940;
 RA Mosckel B., Zinke H., Flach R., Weiss B., Weiler-Guettler H.,
 RA Gassem H.;
 RT "Expression of apolipoprotein A-I in porcine brain endothelium in
 RT vitro.";
 RL J. Neurochem. 62:788-798(1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 34-265.
 RC TISSUE=Brain;
 RX MEDLINE=90132667; PubMed=2105375;
 RA Weiler-Guettler H., Sommerfeldt M., Papandrikopoulou A., Mischek U.,
 RA Bonitz D., Frey A., Grupe M., Scheerer J., Gassem H.G.;
 RT "Synthesis of apolipoprotein A-1 in pig brain microvascular
 RT endothelial cells.";

RL J. Neurochem. 54:444-450(1990).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 105-265, AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RA MEDLINE=93154581; PubMed=8428656; DOI=10.1016/0378-1119(93)90121-I;
 RX Trieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;
 RA "Sequences and expression of the porcine apolipoprotein A-I and C-III
 RT mRNAs";
 RL Gene 123:173-179(1993).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 105-265.
 RX MEDLINE=94085789; PubMed=7916724; DOI=10.1016/0378-1119(93)90105-C;
 RA Trieu V.N., Patel B., Zhan R., Black D.D.;
 RT "Sequence of the porcine apoA-I gene";
 RL Gene 134:267-270(1993).
 RN [6]
 RP PROTEIN SEQUENCE OF 25-265.
 RX MEDLINE=76184721; PubMed=178359;
 RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
 RT "Characterization of the plasma lipoproteins and apoproteins of the
 RT Erythrocybus patas monkey";
 RL Biochemistry 15:1928-1933(1976).
 CC -!- FUNCTION: Participates in the reverse transport of cholesterol
 CC from tissues to the liver for excretion by promoting cholesterol
 CC efflux from tissues and by acting as a cofactor for the lecithin
 CC cholesterol acyltransferase (LCAT).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
 CC chylomicrons. Synthesized predominantly in the intestine and the
 CC liver.
 CC -!- DEVELOPMENTAL STAGE: Liver apoA-I expressed in fetal, newborn and
 CC suckling animals. Intestinal apoA-I only expressed in postpartum
 CC animals.
 CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; L00626; AAA30992.1; -; Genomic_DNA.
 DR EMBL; X69477; CAA49234.1; -; mRNA.
 DR EMBL; X17057; -; NOT ANNOTATED CDS; mRNA.
 DR EMBL; X59414; CAA42050.1; -; mRNA.
 DR PIR; A46018; A46018.
 DR PIR; J70672; J70672.
 DR PIR; S21830; S21830.
 DR PIR; S31394; S31394.
 DR HSSP; P02647; 1AVI.
 DR SMR; P18648; 67-265.
 DR InterPro; IPR000074; ApoA1_A4_E.
 DR PANTHER; PTHR18976; ApoA1_A4_E; 1.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Cholesterol metabolism; Direct protein sequencing; HDL;
 KW Lipid metabolism; Lipid transport; Plasma; Repeat; Signal;
 KW Steroid metabolism; Transport.
 FT SIGNAL 1 18 By similarity.
 FT PROPEP 19 24
 FT CHAIN 25 265 Apolipoprotein A-I.
 FT REPEAT 67 88 1.
 FT REPEAT 89 110 2.
 FT REPEAT 111 121 3 (half-length).
 FT REPEAT 122 142 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 230 8.

FT REPEAT 231 241 9 (half-length).
 FT REPEAT 242 265 10.
 FT REGION 67 265 E -> K (in Ref. 3).
 FT CONFLICT 108 108 Missing (in Ref. 2 and 3).
 FT CONFLICT 143 143 D -> S (in Ref. 4).
 FT CONFLICT 173 173 E -> A (in Ref. 2 and 3).
 FT CONFLICT 180 180 HV -> QL (in Ref. 1 and 6).
 FT CONFLICT 185 186 G -> D (in Ref. 2 and 3).
 FT CONFLICT 209 209 G -> G (in Ref. 4).
 FT CONFLICT 224 224 A -> G (in Ref. 4).
 SQ SEQUENCE 265 AA; 30325 MW; 2C6B578318ECF69C CRC64;
 Query Match 81.1%; Score 1105; DB 1; Length 265;
 Best Local Similarity 80.9%; Pred. No. 4.3e-51;
 Matches 216; Conservative 20; Mismatches 29; Indels 2; Gaps 2;
 Oy 1 MKAAVLTAVLFLTGTGQARHFQWDEPPQSPWDRVKDLATVYDVLDKSDRDYVSQEGS 60
 Db 1 MKAAVLTAVLFLTGTGQARHFQWQDD-PQSPWDRVKDFATVYDVDAIKSDGRDYVAQFEAS 59
 Oy 61 ALGKQLNLKLLDNWDSVTSTFSKLRQQLGPVTOBFWDNLSEKTEGLRQEMSKDLEEVKAK 120
 Db 60 ALGHLNLKLLDNWDSLGSTFTTKVREQLPVTOBFWDNLSEKTEGLRQEMSKDLEEVKK 119
 Oy 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEEMDRAPAHV 180
 Db 120 VQPYLDDFQKKQWQEMELYRQKVAFLGAEFREGARQKQVLEQKLSPLAEELRDLRAHV 179
 Oy 181 DALRTHLAPYSDELRLQRLAARLALKENGARLAETHAKATEHLSLSEKAKPALEDLRQ 240
 Db 180 EALRHQVAPYSDDLRLQRLAARLALKENGARLAETHAKATEHLSLSEKAKPALEDLRQ 238
 Oy 241 GLLPVLESFVSLSALEYTKKLNQ 267
 Db 239 GLLPVLENLKVSLIAIDEASKLNQ 265
 RESULT 7
 APOAL RABIT
 ID APOAL RABIT STANDARD; PRT; 266 AA.
 AC P09809;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).
 GN Name=ApoA1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=22AP AI; TISSUE=Small intestine;
 RX MEDLINE=88082866; PubMed=3121329;
 RA Pan T.C., Hao Q.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,
 RA Kroon P.A., Chao Y.S.;
 RA "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit
 RT apolipoprotein A-I is synthesized in the intestine but not in the
 RT liver.";
 RL Eur. J. Biochem. 170:99-104(1987).
 RN [3]
 RP PROTEIN SEQUENCE OF 25-266.
 RX MEDLINE=87030294; PubMed=3095115;
 RA Yang C., Yang T., Fownall H.J., Gatto A.M. Jr.;
 RA "The primary structure of apolipoprotein A-I from rabbit high-density
 RT lipoprotein.";
 RL Eur. J. Biochem. 160:427-431(1986).


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FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3. (half-length).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 230 8.
FT REPEAT 231 241 9. (half-length).
FT REPEAT 242 265 10. X approximate tandem repeats.
FT REGION 67 265
FT CONFLICT 185 186
SQ SEQUENCE 265 AA; 30276 MW; 06A2681EA2ABA50F CRC64;

Query Match
Best Local Similarity 79.1%; Score 1077; DB 1; Length 265;
Matches 210; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

Qy 1 MKAAVLTAVLFLTGSAHFHQDEPPQSPWDRVKOLATVYVDVLDKSDGRDYVSQFEGS 60
Db 1 MKAVVLTAVLFLTGSAHFHQDD--PQSSWDVVKDFATVYVEAIKSDGRDYVAQFEAS 59

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKRLREQLGPVTFQFMDNLEKTEGLRQEMSKOLEEVKAK 120
Db 60 ALGKQLNLKLLDNWDTLASTLSKVRQLGPVTFQFMDNLEKTEGLRQEMSKOLEEVKAK 119

Qy 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMRDRARAHV 180
Db 120 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMRDRARAHV 179

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 ETLRQLAPYSDDLRLQRLAARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQ 238

Qy 241 GLLPVLESFKVSFLSALSEYTKKLNQ 267
Db 239 GLLPVLESFKVSFLSALSEYTKKLNQ 265

RESULT 9
APOAI MESAU STANDARD; PRT; 264 AA.
AC Q942L4;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).
GN Name=APOAI;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Cricetinae; Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SVrian; TISSUE=Intestine;
RX MEDLINE=90061559; PubMed=9843713;
RA Wu J.Y., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;
RT "Zinc deficiency decreases plasma level and hepatic mRNA abundance of
RL apolipoprotein A-I in rats and hamsters.";
RL Am. J. Physiol. 275:C1516-C1525(1998).
CC -!- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
CC cholesterol acyltransferase (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons.
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC
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use as long as its content is in no way modified and this statement is not
removed.
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DR EMBL; AF046919; AAC98484.1; -; mRNA.
DR HSPF; P02647; IAV1.
DR InterPro; IPR000074; APOA1_A4_E.
DR PANTHER; PTHR18976; APOA1_A4_E; 1.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Cholesterol metabolism; HDL; Lipid metabolism; Lipid transport;
KW Plasma; Repeat; Signal; Steroid metabolism; Transport.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 264
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3. (half-length).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 207 7.
FT REPEAT 208 229 8.
FT REPEAT 230 240 9. (half-length).
FT REPEAT 241 264 10.
FT REGION 67 264
SQ SEQUENCE 264 AA; 30739 MW; 280B22F4C0F0B129 CRC64;

Query Match
Best Local Similarity 74.3%; Score 1012.5; DB 1; Length 264;
Matches 195; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

Qy 1 MKAAVLTAVLFLTGSAHFHQDEPPQSPWDRVKOLATVYVDVLDKSDGRDYVSQFEGS 60
Db 1 MKTVLAVAVLFLTGSAHFHQDD--PQTPWDRVKDFATVYVDVDAVKDSGREYVSQFETS 59

Qy 61 ALGKQLNLKLLDNWDSVTSTFSKRLREQLGPVTFQFMDNLEKTEGLRQEMSKOLEEVKAK 120
Db 60 ALGKQLNLNLENWDTLSTVGRLEQLGPVTFQFMDNLEKTEGLRQEMSKOLEEVKAK 119

Qy 121 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMRDRARAHV 180
Db 120 VQPYLDDFQKKQWQEMELYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMRDRARAHV 179

Qy 181 DALRTHLAPYSDELQRLAARLEALKENGARLAETHAKATEHLSTLSEKAKPALEDLRQ 240
Db 180 DALRTKMTPTPSDQMDRLAERLAQLKDS--PTLAEYHTTKAADHLKAFGEKAKPALEDLRQ 237

Qy 241 GLLPVLESFKVSFLSALSEYTKKLNQ 267
Db 238 GLMPVFESFKTRIMSMVVEASKKLNQ 264

RESULT 10
APOAI TUPGB STANDARD; PRT; 265 AA.
AC O18759;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).
GN Name=APOAI;
OS Tupiaia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupiaia.
OX NCBI_TaxID=37347;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
RT "Cloning and sequencing of tree shrew apolipoprotein AI cDNA.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
```

```
CC cholesterol acyltransferase (LCAT) (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons (By similarity).
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AF005638; AAB82326.1; -; mRNA.
CC HSSP: P02647; 1AV1.
CC InterPro: IPR000074; ApoA1_A4_E.
CC Pfam: PTHR18976; ApoA1_A4_E; 1.
CC KW Cholesterol metabolism; HDL; Lipid metabolism; Lipid transport;
CC Plasma; Repeat; Signal; Steroid metabolism; Transport.
CC FT SIGNAL 1 18 By similarity.
CC FT PROPEP 19 24 By similarity.
CC FT CHAIN 25 265 Apolipoprotein A-I.
CC FT REPEAT 67 88 1.
CC FT REPEAT 89 110 2.
CC FT REPEAT 111 121 3 (half-length).
CC FT REPEAT 122 143 4.
CC FT REPEAT 144 165 5.
CC FT REPEAT 166 187 6.
CC FT REPEAT 188 209 7.
CC FT REPEAT 210 231 8.
CC FT REPEAT 232 242 9 (half-length).
CC FT REPEAT 243 265 10.
CC FT REGION 67 265 10 X approximate tandem repeats.
CC SEQUENCE 265 AA; 30332 MW; 60076BC39FAEA165 CRC64;
Query Match 71.6%; Score 975.5; DB 1; Length 265;
Best Local Similarity 69.7%; Pred. No. 3.1e-44;
Matches 184; Conservative 38; Mismatches 41; Indels 1; Gaps 1;
QY 1 MKAAVLTAVLFLTGSQARHFHWQDEPPQSPWDRVKLATVYVDVKDSGRDYVSQFEGS 60
DB 1 MKAVVLTAVLFLTGSQARHFHWQDE-PQSSWDRVRDLANVYVDVAVKSGREYVSQLEAS 59
QY 61 ALGKQLNKLNDWDSVTSFKLREQLGPTVQBFWDNLEKETEGRLQEMSKDLVEVKAK 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 119
60 ALGKQLNKLNDWNTLTGTTQKVHHLGVAQEFWEKLEKETEBELREINKLLEDDVRQK 119
QY 121 VQPLDQKQWQEMELYRQKVEPLRAELQEGAROKLHELQKLSPLGEEWRDRARAHV 180
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 179
120 TOPFLDEIQKQWQEDLERYRQKVEPLSAQLREGAROKLMEIQVTPLGEDLRDSVRAYA 179
QY 181 DALRTHLAPYSDELQRLAARLEALKKENGARLARAEYHAKATEHLSTLSEKAKPALEDLRQ 240
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 239
180 DTLRTQLAPYSEQWKTGRLAEIAKEGSGSLAEYHAKASEQLSALGEKAKPVLIEDIHQ 239
QY 241 GLLPVLESFKVSVLSALREYTNKL 264
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 263
240 GLMPWESFKTGVLNVIDEAAKKL 263
RESULT 11
ID Q8HZ96_9PRIM PRELIMINARY; PRT; 191 AA.
AC Q8HZ96;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Apolipoprotein A-I (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Gorilla.
OX NCBI_TaxID=9593;
Query Match 70.6%; Score 962; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 1.2e-43;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RN NUCLEOTIDE SEQUENCE.
RP O'Nuigin C., Tichy H., Klein J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AY092007; AAM76624.1; -; Genomic_DNA.
HSSP: P02647; 1AV1.
SMR: Q8HZ96; 31-191.
DR GO: 0005576; C:extracellular region; IEA.
DR GO: 0008289; F:lipid binding; IEA.
DR GO: 0006869; P:lipid transport; IEA.
DR GO: 0042157; P:lipoprotein metabolism; IEA.
DR InterPro: IPR000074; ApoA1_A4_E.
DR Pfam: PF01442; Apolipoprotein_1.
KW Lipoprotein.
FT NON_TER 1 191
FT NON_TER 191 191
SQ SEQUENCE 191 AA; 22087 MW; 2D30919874C8F0F4 CRC64;
Query Match 70.6%; Score 962; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 1.2e-43;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 38 LATVYVDVLKDSGRDYVSQFEGSALGKQLNKLNDWDSVTSFKLREQLGPTVQBFWD 97
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
1 LATVYVDVLKDSGRDYVSQFEGSALGKQLNKLNDWDSVTSFKLREQLGPTVQBFWD 60
QY 98 NLEKETEGRLQEMSKDLVEVKAKVQPYLDDPQKQWQEMELYRQKVEPLRAELQEGAROK 157
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
61 NLEKETEGRLQEMSKDLVEVKAKVQPYLDDPQKQWQEMELYRQKVEPLRAELQEGAROK 120
QY 158 LHELQKLSPLGEEWRDRARAHVDALRTHLAPYSDELQRLAARLEALKKENGARLARAEYH 217
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 217
121 LHELQKLSPLGEEWRDRARAHVDALRTHLAPYSDELQRLAARLEALKKENGARLARAEYH 180
QY 218 AKATEHLSTLS 228
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 191
181 AKATEHLSTLS 191
RESULT 12
ID Q8HZ97_PANTR PRELIMINARY; PRT; 191 AA.
AC Q8HZ97;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Apolipoprotein A-I (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN NUCLEOTIDE SEQUENCE.
RP O'Nuigin C., Tichy H., Klein J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AY092007; AAM76624.1; -; Genomic_DNA.
HSSP: P02647; 1AV1.
SMR: Q8HZ97; 31-191.
DR GO: 0005576; C:extracellular region; IEA.
DR GO: 0008289; F:lipid binding; IEA.
DR GO: 0006869; P:lipid transport; IEA.
DR GO: 0042157; P:lipoprotein metabolism; IEA.
DR InterPro: IPR000074; ApoA1_A4_E.
DR Pfam: PF01442; Apolipoprotein_1.
KW Lipoprotein.
FT NON_TER 1 191
FT NON_TER 191 191
SQ SEQUENCE 191 AA; 22087 MW; 2D30919874C8F0F4 CRC64;
Query Match 70.6%; Score 962; DB 2; Length 191;
Best Local Similarity 99.0%; Pred. No. 1.2e-43;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 38 LATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNWDVSTSTFKLREQLGPTVQSFWD 97
Db 1 LATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNWDVSTSTFKLREQLGPTVQSFWD 60
QY 98 NLEKETEGLOEMSKDLEEVAKVQPYLDDFKKQWEEMELYRQKVEPLRAELOEGARQK 157
Db 61 NLEKETEGLOEMSKDLEEVAKVQPYLDDFKKQWEEMELYRQKVEPLRAELOEGARQK 120
QY 158 LHELQEKLSPLGEEMRDARAHVDALRTHLAPYSDELQRLAARLEALKENGGLARLAEYH 217
Db 121 LHELQEKLSPLGEEMRDARAHVDALRTHLAPYSDELQRLAARLEALKENGGLARLAEYH 180
QY 218 AKATEHLSLTS 228
Db 181 AKATEHLSLTS 191
RESULT 13
Q8BPD5_PONPY PRELIMINARY; PRT; 191 AA.
AC Q8BZ95
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OS Pongo pygmaeus (Orangutan)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN NUCLEOTIDE SEQUENCE.
RA O'Nigin C., Tichy H., Klein J.;
RP Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY092009; AAM76626.1; -; Genomic_DNA.
DR HSSP; P02647; IAV1.
DR SMR; Q8BZ95; 31-191.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0006889; F:lipid transport; IEA.
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR InterPro; IPR000074; ApoA1_A4_E.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 191
FT NON_TER 191
SQ SEQUENCE 191 AA; 22128 MW; D8D0671444C13725 CRC64;
Query Match 69.5%; Score 947; DB 2; Length 191;
Best Local Similarity 96.9%; Pred. No. 7.2e-43;
Matches 185; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 38 LATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNWDVSTSTFKLREQLGPTVQSFWD 97
Db 1 LATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNWDVSTSTFKLREQLGPTVQSFWD 60
QY 98 NLEKETEGLOEMSKDLEEVAKVQPYLDDFKKQWEEMELYRQKVEPLRAELOEGARQK 157
Db 61 NLEKETEGLOEMSKDLEEVAKVQPYLDDFKKQWEEMELYRQKVEPLRAELOEGARQK 120
QY 158 LHELQEKLSPLGEEMRDARAHVDALRTHLAPYSDELQRLAARLEALKENGGLARLAEYH 217
Db 121 LHELQEKLSPLGEEMRDARAHVDALRTHLAPYSDELQRLAARLEALKENGGLARLAEYH 180
QY 218 AKATEHLSLTS 228
Db 181 AKATEHLSLTS 191
RESULT 14
Q8BPD5_MOUSE PRELIMINARY; PRT; 264 AA.
ID Q8BPD5_MOUSE

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AC Q8BPD5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 18 days pregnant adult female placenta and extra
DE embryonic tissue cDNA, RIKEN full-length enriched library,
DE clone:3830418K20 product:apolipoprotein A-I, full insert
DE sequence.
GN Name=Apoal;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RA Carninci P., Hayashizaki Y.;
RP Carninci P., Hayashizaki Y.;
RL Meth. Enzymol. 303:19-44(1999).
[2]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland Y., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bargh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
RC The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
RC MEDLINE=20493974; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Carninci P., Hayashizaki Y.;
RL Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

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RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";

RL
 RN Genome Res. 10:1757-1771 (2000).

[6]

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta and extra embryonic tissue;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saichoh K., Sakai C., Sakai C., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK076187; BAC36241.1; -; mRNA.

DR HSSP; P02647; 1AV1.

DR MGI; MGI:88049; ApoA1.

DR GO; GO:0005615; C:extracellular space; IDA.

DR GO; GO:0005319; F:lipid transporter activity; IMP.

DR GO; GO:0030300; P:regulation of cholesterol absorption; IDA.

DR InterPro; IPR000074; ApoA1_A4_E.

DR Pfam; PF01442; Apolipoprotein; 1.

KW Lipoprotein.

SQ SEQUENCE 264 AA; 30615 MW; 5E33FF201963583B CRC64;

Query Match 66.5%; Score 905.5; DB 2; Length 264;

Best Local Similarity 65.2%; Pred. No. 1.6e-40;

Matches 174; Conservative 41; Mismatches 49; Indels 3; Gaps 2;

QY 1 MKAAVLTLAVLPLTGSQARHFQDPPQSPMDRVKDLATVVDVLDKSGRDYVSQFSGS 60
 DB 1 MKAVLVALVPLTGSQARHFQDPPQSPMDRVKDLATVVDVLDKSGRDYVSQFSGS 59
 QY 61 ALGKQLNKLNDWDSVTSFTSKLREQLGQVPTQEFWDNLEKETGLRQEMSKDLFEVAK 120
 DB 60 SLGQQLNKLNDWDSVTSFTSKLREQLGQVPTQEFWDNLEKETGLRQEMSKDLFEVAK 119
 QY 121 VQPYLDDFQKQWQEMELYRQKVEPLRAELOEGARQKLEHQLGSEWEDPARAHV 180
 DB 120 VQPYLDDFQKQWQEMELYRQKVEPLRAELOEGARQKLEHQLGSEWEDPARAHV 179
 QY 181 DALRTHLAPYSDELQRLAARLEALKENGARLAHYHAKATHEHLSTLSEKAKPALEDLRQ 240
 DB 180 DSLRTQLAPHSPQMSRESLAQLAELKSN--PTLNEYHTRAKTHLKTGLGEKAPPALEDLRH 237

QY 241 GLLPVLSPKVSFLSALBEYTKKLNQ 267

DB 238 SLMPMLETLTKQVQSVIDKASSETLTAQ 264

RESULT 15

AP0A1 MOUSE

ID AP0A1 MOUSE STANDARD; PRT; 264 AA.

AC Q00623;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).

GN Name=ApoA1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=92281682; PubMed=1596360;

RA Stoffel W., Mueller R., Binczek E., Hofmann K.;

RT "Mouse apolipoprotein AI. cDNA-derived primary structure, gene

organisation and complete nucleotide sequence.";

RL Biol. Chem. Hoppe-Seyler 373:187-193 (1992).

RN [2]

NUCLEOTIDE SEQUENCE.

RX MEDLINE=93122774; PubMed=1478650;

RA Januzzi J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;

RT "Characterization of the mouse apolipoprotein ApoA-1/ApoC-3 gene

locus: genomic, mRNA, and protein sequences with comparisons to other

species.";

RL Genomics 14:1081-1088 (1992).

RN [3]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Liver;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,

RA Klausner S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Paney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Participates in the reverse transport of cholesterol
 from tissues to the liver for excretion by promoting cholesterol
 efflux from tissues and by acting as a cofactor for the lecithin

cholesterol acyltransferase (LCAT).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in

chylomicrons.

CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

DR EMBL; X64262; CAA45560.1; -; mRNA.

DR EMBL; X64263; CAA45561.1; -; Genomic DNA.

DR EMBL; L04149; -; NOT ANNOTATED CDS; Genomic_DNA.

DR EMBL; L04151; -; NOT ANNOTATED CDS; mRNA.

DR EMBL; BC012253; AAH12253.1; -; mRNA.

DR EMBL; BC019837; AAH19837.1; -; mRNA.

DR PIR; S22420; S22420.

DR HSSP; P02647; 1AV1.

DR SWISS-2DPAGE; Q00623; MOUSE.

DR Ensembl; ENSMUSG0000032083; Mus musculus.

DR MGI; MGI:88049; ApoA1.

DR GO; GO:0005615; C:extracellular space; IDA.

DR GO; GO:0005319; F:lipid transporter activity; IMP.

DR GO; GO:0030300; P:regulation of cholesterol absorption; IDA.

DR InterPro; IPR000074; ApoA1_A4_E.

DR PANTHER; PTHR18976; ApoA1_A4_E; 1.

DR Pfam; PF01442; Apolipoprotein; 1.

KW Cholesterol metabolism; HDL; lipid metabolism; Lipid transport;

Plasma; Repeat; Signal; Steroid metabolism; Transport.

SIGNAL 1 18 By similarity.

FT PROPEP 19 24 By similarity.

FT CHAIN 25 264 Apolipoprotein A-I.

FT REPEAT 67 88 1.

FT REPEAT 89 110 2.

